

SEQUENCE LISTING

<110> Chang, Chawnshang

<120> Androgen Receptor Coregulators

<130> 21108.0011U6

<140> 10/517,155

<141> 2005-01-06

<150> PCT/US03/17937

<151> 2003-06-06

<150> US 60/387,087

<151> 2002-06-06

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<222> (40)...(1464)

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<222> (1120)...(1452)

<223> Coding sequence and polypeptide region for the
C-terminal domain

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<222> (697)...(834)

<223> Coding sequence and polypeptide region which may
form a cystein-rich RING finger motif

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<222> (964)...(1089)

<223> Coding sequence and polypeptide region for a
cystein-rich B box like structure

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Arg	Glu	Ala	Gln	Glu	Asp	Glu	Leu	Leu	Ala	Leu	Ala	Ser	Ile	Tyr	Asp	
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tca aat gag tgt ctc cag aat agt ggc ttt gaa tac acc att tgc ttt Ser Asn Glu Cys Leu Gln Asn Ser Gly Phe Glu Tyr Thr Ile Cys Phe 55 60 65	246
ctg cct cca ctt gtg ctg aac ttt gaa ctg cca cca gat tat cca tcc Leu Pro Pro Leu Val Leu Asn Phe Glu Leu Pro Pro Asp Tyr Pro Ser 70 75 80 85	294
tct tcc cca cct tca ttc aca ctt agt ggc aaa tgg ctg tca cca act Ser Ser Pro Pro Ser Phe Thr Leu Ser Gly Lys Trp Leu Ser Pro Thr 90 95 100	342
cag cta tct gct cta tgc aag cac tta gac aac cta tgg gaa gaa cac Gln Leu Ser Ala Leu Cys Lys His Leu Asp Asn Leu Trp Glu Glu His 105 110 115	390
cgt ggc agc gtg gtc ctg ttt gcc tgg atg caa ttt ctt aag gaa gag Arg Gly Ser Val Val Leu Phe Ala Trp Met Gln Phe Leu Lys Glu Glu 120 125 130	438
acc cta gca tac ttg aat att gtc tct cct ttt gag ctc aag att ggt Thr Leu Ala Tyr Leu Asn Ile Val Ser Pro Phe Glu Leu Lys Ile Gly 135 140 145	486
tct cag aaa aaa gtg cag aga agg aca gct caa gct tct ccc aac aca Ser Gln Lys Lys Val Gln Arg Arg Thr Ala Gln Ala Ser Pro Asn Thr 150 155 160 165	534
gag cta gat ttt gga gga gct gct gga tct gat gta gac caa gag gaa Glu Leu Asp Phe Gly Gly Ala Ala Gly Ser Asp Val Asp Gln Glu Glu 170 175 180	582
att gtg gat gag aga gca gtg cag gat gtg gaa tca ctg tca aat ctg Ile Val Asp Glu Arg Ala Val Gln Asp Val Glu Ser Leu Ser Asn Leu 185 190 195	630
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agt gaa tgc atg tac ttc ttg gag tgc agg cat gtg tac tgc aaa gcc Ser Glu Cys Met Tyr Phe Leu Glu Cys Arg His Val Tyr Cys Lys Ala 230 235 240 245	774
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ctt ctc ctc cag tcc tcc ttg gac ctg atg gca gat gtg gtg tac tgc Leu Leu Leu Gln Ser Ser Leu Asp Leu Met Ala Asp Val Val Tyr Cys 295 300 305	966
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ctt ttg gat caa agg tat ggt aag aga gtg att cag aag gca ctg gaa Leu Leu Asp Gln Arg Tyr Gly Lys Arg Val Ile Gln Lys Ala Leu Glu 375 380 385	1206
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gat gag gta gaa gac tag ttaactactg ctcaagatat ttaactactg Asp Glu Val Glu Asp *	1494
ctcaagatat ggaagtggat tgtttttccc taatcttccg tcaagtacac aaagtaactt tgcgggatat ttaggggtact attcattcac tcttcctgcg tagaagatat ggaagaacga ggtttatatt ttcatgtggt actactgaag aagggtgcatt gatacatattt taaatgtaag ttgagaaaaa ttataagcc aaaggttcag aaaattaaac tacagaa	1554 1614 1674 1721

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Tyr	Thr	Ile	Cys	Phe	Leu	Pro	Pro	Leu	Val	Leu	Asn	Phe	Glu	Leu	Pro
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Val	Ala	Thr	Pro	Gly	Gln	Val	Lys	Glu	Leu	Val	Glu	Ala	Glu	Leu	Phe
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Glu	Pro	Gly	Cys	Thr	Met	Gly	Ile	Cys	Ser	Ser	Cys	Asn	Phe	Ala	Phe
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Cys	Asn	Lys	Met	Thr	Cys	Thr	Gly	Cys	Met	Gln	Tyr	Phe	Cys	Trp	Ile
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 Pro Pro Pro Ser Tyr Gly His Gln Pro Thr Gly Gln Ser Gly Glu Ser
 20 25 30
 tca gga gcc tcg ggg gac aag gac cac ctg tac agc acg gta tgc aag 144
 Ser Gly Ala Ser Gly Asp Lys Asp His Leu Tyr Ser Thr Val Cys Lys
 35 40 45

cct cgg tcc cca aag cct gca gcc ccg gcc gcc cct cca ttc tcc tct Pro Arg Ser Pro Lys Pro Ala Ala Pro Ala Ala Pro Pro Phe Ser Ser 50 55 60	192
tcc agc ggt gtc ttg ggt acc ggg ctc tgt gag cta gat cgg ttg ctt Ser Ser Gly Val Leu Gly Thr Gly Leu Cys Glu Leu Asp Arg Leu Leu 65 70 75 80	240
cag gaa ctt aat gcc act cag ttc aac atc aca gat gaa atc atg tct Gln Glu Leu Asn Ala Thr Gln Phe Asn Ile Thr Asp Glu Ile Met Ser 85 90 95	288
cag ttc cca tct agc aag gtg gct tca gga gag cag aag gag gac cag Gln Phe Pro Ser Ser Lys Val Ala Ser Gly Glu Gln Lys Glu Asp Gln 100 105 110	336
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ctc cca aag gct tct gcc acc tca gcc act ctg gag ctg gat aga ctg Leu Pro Lys Ala Ser Ala Thr Ser Ala Thr Leu Glu Leu Asp Arg Leu 130 135 140	432
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Pro Arg Ser Pro Lys Pro Ala Ala Pro Ala Ala Pro Phe Ser Ser 50 55 60
Ser Ser Gly Val Leu Gly Thr Gly Leu Cys Glu Leu Asp Arg Leu Leu 65 70 75 80
Gln Glu Leu Asn Ala Thr Gln Phe Asn Ile Thr Asp Glu Ile Met Ser 85 90 95

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Ser	Glu	Asp	Lys	Lys	Arg	Pro	Ser	Leu	Pro	Ser	Ser	Pro	Ser	Pro	Gly	115	120	125
Leu	Pro	Lys	Ala	Ser	Ala	Thr	Ser	Ala	Thr	Leu	Glu	Leu	Asp	Arg	Leu	130	135	140
Met	Ala	Ser	Leu	Pro	Asp	Phe	Arg	Val	Gln	Asn	His	Leu	Pro	Ala	Ser	145	150	155
Gly	Pro	Thr	Gln	Pro	Pro	Val	Val	Ser	Ser	Thr	Asn	Glu	Gly	Ser	Pro	165	170	175
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Gly	Leu	Cys	Gly	Ser	Cys	Asn	Lys	Pro	Ile	Ala	Gly	Gln	Val	Val	Thr	210	215	220
Ala	Leu	Gly	Arg	Ala	Trp	His	Pro	Glu	His	Phe	Val	Cys	Gly	Gly	Cys	225	230	235
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Phe	Cys	Pro	Glu	Cys	Tyr	Phe	Glu	Arg	Phe	Ser	Pro	Arg	Cys	Gly	Phe	260	265	270
Cys	Asn	Gln	Pro	Ile	Arg	His	Lys	Met	Val	Thr	Ala	Leu	Gly	Thr	His	275	280	285
Trp	His	Pro	Glu	His	Phe	Cys	Cys	Val	Ser	Cys	Gly	Glu	Pro	Phe	Gly	290	295	300
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Gly	Ser	Leu	Cys	Pro	Thr	Cys	Gly	Leu	Pro	Val	Thr	Gly	Arg	Cys	Val	385	390	395
Ser	Ala	Leu	Gly	Arg	Arg	Phe	His	Pro	Asp	His	Phe	Ala	Cys	Thr	Phe	405	410	415
Cys	Leu	Arg	Pro	Leu	Thr	Lys	Gly	Ser	Phe	Gln	Glu	Arg	Ala	Gly	Lys	420	425	430
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Gln Phe Lys Leu Val Leu Val Gly Asp Gly Gly Thr Gly Lys Thr Thr	
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Phe Val Lys Arg His Leu Thr Gly Glu Phe Glu Lys Lys Tyr Val Ala	
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acc ttg ggt gtt gag gtt cat ccc cta gtg ttc cac acc aac aga gga	195
Thr Leu Gly Val Glu Val His Pro Leu Val Phe His Thr Asn Arg Gly	
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cct att aag ttc aat gta tgg gac aca gcc ggc cag gag aaa ttc ggt	243
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Arg Asp Leu Val Arg Val Cys Glu Asn Ile Pro Ile Val Leu Cys Gly	
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Asn Lys Val Asp Ile Lys Asp Arg Lys Val Lys Ala Lys Ser Ile Val	
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Phe His Arg Lys Lys Asn Leu Gln Tyr Tyr Asp Ile Ser Ala Lys Ser	
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Asn Tyr Asn Phe Glu Lys Pro Phe Leu Trp Leu Ala Arg Lys Leu Ile	
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Gly Asp Pro Asn Leu Glu Phe Val Ala Met Pro Ala Leu Ala Pro Pro	
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Glu Val Val Met Asp Pro Ala Leu Ala Ala Gln Tyr Glu His Asp Leu	
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Glu Val Ala Gln Thr Thr Ala Leu Pro Asp Glu Asp Asp Asp Leu	
205 210 215	
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Gly Glu Phe Glu Lys Lys Tyr Val Ala Thr Leu Gly Val Glu Val His
 35          40          45
Pro Leu Val Phe His Thr Asn Arg Gly Pro Ile Lys Phe Asn Val Trp
 50          55          60
Asp Thr Ala Gly Gln Glu Lys Phe Gly Gly Leu Arg Asp Gly Tyr Tyr
 65          70          75          80
Ile Gln Ala Gln Cys Ala Ile Ile Met Phe Asp Val Thr Ser Arg Val
 85          90          95
Thr Tyr Lys Asn Val Pro Asn Trp His Arg Asp Leu Val Arg Val Cys
100          105          110
Glu Asn Ile Pro Ile Val Leu Cys Gly Asn Lys Val Asp Ile Lys Asp
115          120          125
Arg Lys Val Lys Ala Lys Ser Ile Val Phe His Arg Lys Lys Asn Leu
130          135          140
Gln Tyr Tyr Asp Ile Ser Ala Lys Ser Asn Tyr Asn Phe Glu Lys Pro
145          150          155          160
Phe Leu Trp Leu Ala Arg Lys Leu Ile Gly Asp Pro Asn Leu Glu Phe
165          170          175
Val Ala Met Pro Ala Leu Ala Pro Pro Glu Val Val Met Asp Pro Ala
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Leu Ala Ala Gln Tyr Glu His Asp Leu Glu Val Ala Gln Thr Thr Ala
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acc gcc gcc gct gcc gcc gcg gaa ccc ccg gca ccg ccg ccg ccg ccc	218
Thr Ala Ala Ala Ala Ala Ala Glu Pro Pro Ala Pro Pro Pro Pro Pro	
15 20 25	
cct cct gag gag gac cca gag cag gac agc ggc ccg gag gac ctg cct	266
Pro Pro Glu Glu Asp Pro Glu Gln Asp Ser Gly Pro Glu Asp Leu Pro	
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Leu Val Arg Leu Glu Phe Glu Glu Thr Glu Glu Pro Asp Phe Thr Ala	
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Leu Cys Gln Lys Leu Lys Ile Pro Asp His Val Arg Glu Arg Ala Trp	
60 65 70 75	
tta act tgg gag aaa gtt tca tct gtg gat gga gta ttg gga ggt tat	410
Leu Thr Trp Glu Lys Val Ser Ser Val Asp Gly Val Leu Gly Gly Tyr	
80 85 90	
att caa aag aaa aag gaa ctg tgg gga atc tgt atc ttt att gca gca	458
Ile Gln Lys Lys Lys Glu Leu Trp Gly Ile Cys Ile Phe Ile Ala Ala	
95 100 105	
gtt gac cta gat gag atg tcg ttc act ttt act gag cta cag aaa aac	506
Val Asp Leu Asp Glu Met Ser Phe Thr Phe Thr Glu Leu Gln Lys Asn	
110 115 120	
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Ile Glu Ile Ser Val His Lys Phe Phe Asn Leu Leu Lys Glu Ile Asp	
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acc agt acc aaa gtt gat aat gct atg tca aga ctg ttg aag aag tat	602
Thr Ser Thr Lys Val Asp Asn Ala Met Ser Arg Leu Leu Lys Lys Tyr	
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Asp Val Leu Phe Ala Leu Phe Ser Lys Leu Glu Arg Thr Cys Glu Leu	
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Ile Tyr Leu Thr Gln Pro Ser Ser Ser Ile Ser Thr Glu Ile Asn Ser	
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Ala Leu Val Leu Lys Val Ser Trp Ile Thr Phe Leu Leu Ala Lys Gly	
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<210> 8

<211> 928

<212> PRT

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35          40          45
Phe Glu Glu Thr Glu Glu Pro Asp Phe Thr Ala Leu Cys Gln Lys Leu
50          55          60
Lys Ile Pro Asp His Val Arg Glu Arg Ala Trp Leu Thr Trp Glu Lys
65          70          75          80
Val Ser Ser Val Asp Gly Val Leu Gly Gly Tyr Ile Gln Lys Lys Lys
85          90          95
Glu Leu Trp Gly Ile Cys Ile Phe Ile Ala Ala Val Asp Leu Asp Glu
100         105         110
Met Ser Phe Thr Phe Thr Glu Leu Gln Lys Asn Ile Glu Ile Ser Val
115         120         125
His Lys Phe Phe Asn Leu Leu Lys Glu Ile Asp Thr Ser Thr Lys Val
130         135         140
Asp Asn Ala Met Ser Arg Leu Leu Lys Lys Tyr Asp Val Leu Phe Ala
145         150         155         160
Leu Phe Ser Lys Leu Glu Arg Thr Cys Glu Leu Ile Tyr Leu Thr Gln
165         170         175
Pro Ser Ser Ser Ile Ser Thr Glu Ile Asn Ser Ala Leu Val Leu Lys
180         185         190
Val Ser Trp Ile Thr Phe Leu Leu Ala Lys Gly Glu Val Leu Gln Met
195         200         205

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Gln	Asn	Arg	Ser	Ala	Arg	Ile	Ala	Lys	Gln	Leu	Glu	Asn	Asp	Thr	Arg
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Ile	Ile	Glu	Val	Leu	Cys	Lys	Glu	His	Glu	Cys	Asn	Ile	Asp	Glu	Val
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Lys	Asn	Val	Tyr	Phe	Lys	Asn	Phe	Ile	Pro	Phe	Met	Asn	Ser	Leu	Gly
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Pro	Leu	Lys	Ser	Thr	Ser	Leu	Ser	Leu	Phe	Tyr	Lys	Lys	Val	Tyr	Arg
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Leu	Gln	Tyr	Ala	Ser	Thr	Arg	Pro	Pro	Thr	Leu	Ser	Pro	Ile	Pro	His
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865					870					875					880
Gly	Ser	Asp	Glu	Ala	Asp	Gly	Ser	Lys	His	Leu	Pro	Gly	Glu	Ser	Lys
			885						890					895	
Phe	Gln	Gln	Lys	Leu	Ala	Glu	Met	Thr	Ser	Thr	Arg	Thr	Arg	Met	Gln
			900					905					910		
Lys	Gln	Lys	Met	Asn	Asp	Ser	Met	Asp	Thr	Ser	Asn	Lys	Glu	Glu	Lys
		915					920					925			

<210> 9
 <211> 30
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: note =
 Oligonucleotide

<400> 9
 ttctgtagtt taatttttctg aacctttggc

30

<210> 10
 <211> 27
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: note =
 synthetic construct

<400> 10
 tcagccgaag agcttcagga agcaggg

27

<210> 11
 <211> 32
 <212> PRT
 <213> Homo sapien

<220>

<221> VARIANT

<222> 2-3, 6-13, 15, 17-18, 20-21, 23-28, 30-31

<223> Xaa can be any amino acid

<400> 11

Cys	Xaa	Xaa	Cys	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Cys	Xaa	His
1				5					10						15	
Xaa	Xaa	Cys	Xaa	Xaa	Cys	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Cys	Xaa	Xaa	Cys	
			20					25						30		

<210> 12

<211> 50

<212> PRT

<213> Homo sapien

<220>

<221> VARIANT

<222> 2-3, 5-20, 22-23, 25-26, 28-29, 31-46, 48-49

<223> Xaa can be any amino acid

<400> 12

Cys	Xaa	Xaa	Cys	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa
1				5					10					15		
Xaa	Xaa	Xaa	Xaa	His	Xaa	Xaa	Cys	Xaa	Xaa	Cys	Xaa	Xaa	Cys	Xaa	Xaa	
			20					25					30			
Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Cys	Xaa	
			35				40					45				
Xaa	Cys															
	50															

<210> 13

<211> 1497

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence; note =
synthetic construct

<400> 13

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ggggagcggg	gaggggaatac	ctaagagcaa	ttggtagctg	gtacttctaa	tgcctcttcc	120
tcctccaacc	tccaagagtc	tgttttggga	ttgggttcag	gaatgaaatt	ctgcctgtgc	180
taacctcctg	gggagccggt	agacttgctt	gttaaaaatc	gcttctgctt	ttggagccta	240
aagcccgggt	ccgaaaaaca	agtggatatt	aggggaaaga	ggggtcttca	aaggctacag	300
tgagtcattc	cagccttcaa	ccatactacg	ccagcactac	gttctctaaa	gccactctgc	360
gctagcttgc	ggtgagggga	ggggagaaaa	ggaaaaggga	ggggagggga	ggggagggag	420
aaaggaggtg	ggaaggcaga	gaggccggct	gcggggggcg	gaccgactca	caaactgttc	480
gatttcgttt	ccacctccca	gcgccccctc	ggagatccct	aggagccagc	ctgctgggag	540
aaccagaggg	tccggagcaa	acctggaggc	tgagagggca	tcagagggga	aaagactgag	600
ctagccactc	cagtgccata	cagaagctta	agggacgcac	cacgccagcc	ccagcccagc	660
gacagccaac	gcctgttgca	gagcggcggc	ttcgaagccg	ccgcccagga	gctgcccttt	720
cctcttcggt	gaagtgttcta	aaagctgcgg	gagactcaga	ggaagcaagg	aaagtgtccg	780
gtaggactac	ggctgccttt	gtcctcttcc	cctctaccct	tacccctctc	tgggtccctc	840
ctccaggagc	tgactaggca	ggctttcttg	ccaacctctc	cccctacacc	cccagctctg	900
ccagccaggt	tgcacagagg	taaaactccct	ttggctgaga	gtaggggagc	ttgttgca	960
ttgcaaggaa	ggcttttggt	agcccagaga	ctgaggagca	acagcacgcc	caggagagtc	1020
cctgggtcca	ggttctcgcc	cctgcacctc	ctcctgcccc	cccctcacc	tgtgtgtggt	1080
gttagaaatg	aaaagatgaa	aaggcagcta	gggtttcagt	agtcgaaagc	aaaacaaaag	1140
ctaaaagaaa	acaaaaagaa	aatagcccag	ttcttatttg	cacctgcttc	agtggacttt	1200
gaatttgtaa	ggcagaggat	ttcccccttt	ccctcccgtc	aaggtttgag	catcttttaa	1260

tctgttcttc	aagtatttag	agacaaactg	tgtaagtagc	agggcagatc	ctgtcttgcg	1320
cgtgccttcc	tttactggag	actttgaggt	tatctgggca	ctccccccac	ccaccccccc	1380
tcttgcaagt	tttcttcccc	ggagcttccc	gcaggtgggc	agctagctgc	agatactaca	1440
tcatacgtca	ggagaactct	tcagagcaag	agacgaggag	gcaggataag	ggaattc	1497

<210> 14
 <211> 600
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence; note =
 synthetic construct

<400> 14	
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tcaggagact	
ctcccttctg	
cttgtcctgg	
tgggcccctgg	120
ggggagcggg	
gaggggaatac	
ctaagagcaa	
ttggtagctg	
gtacttctaa	
tgcctcttcc	180
tcttccaacc	
tccaagagtc	
tggtttggga	
ttgggttcag	
gaatgaaatt	
ctgacctgtgc	240
taacctcctg	
gggagccggg	
agacttgtct	
gttaaaaatc	
gcttctgctt	
ttggagccta	300
aagcccgggt	
ccgaaaaaca	
agtggatatt	
aggggaaaga	
ggggctctca	
aaggctacag	360
tgagtcattc	
cagccttcaa	
ccatactacg	
ccagcactac	
gttctctaaa	
gccactctgc	420
gctagcttgc	
ggtgagggga	
ggggagaaaa	
ggaaagggga	
ggggagggga	
ggggagggag	480
aaaggaggtg	
ggaaggcaga	
gaggccggct	
gcgggggcgg	
gaccgactca	
caaactgttc	540
gatttcgttt	
ccacctccca	
gcgccccctc	
ggagatccct	
aggagccagc	
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aaccagaggg	
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acctggaggc	
tgagagggca	
tcagagggga	
aaagactgag	

<210> 15
 <211> 359
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence; note =
 synthetic construct

<400> 15	
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agtgttctgt	
tctctttttg	
taatcttgga	
atctttttgt	
gctctaaata	120
caattaaaaa	
tggcagaaac	
ttgtttgttg	
gaatacatgt	
gtgactcttg	
gtttgtctct	180
gcgtctggct	
ttagaaatgt	
catccattgt	
gtaaaatact	
ggcttggttg	
tctgccagct	240
aaaacttgcc	
acagccccctg	
ttgtgactgc	
aggctcaagt	
tattgttaac	
aaagagcccc	300
aagaaaagct	
gctaattgtc	
tcttatcacc	
attgttaatt	
tgtaaaaaca	
taaaacaatc	359
taaaatttca	
gatgaatgtc	
atcagagtgc	
ttttcattag	
ctctttttat	
tggctgtct	

<210> 16
 <211> 899
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence; note =
 synthetic construct

<400> 16	
Met Glu Val Gln Leu Gly Leu Gly Arg Val Tyr Pro Arg Pro Pro Ser	
1 5 10 15	
Lys Thr Tyr Arg Gly Ala Phe Gln Asn Leu Phe Gln Ser Val Arg Glu	
20 25 30	
Ala Ile Gln Asn Pro Gly Pro Arg His Pro Glu Ala Ala Asn Ile Ala	
35 40 45	
Pro Pro Gly Ala Cys Leu Gln Gln Arg Gln Glu Thr Ser Pro Arg Arg	
50 55 60	

Arg	Arg	Arg	Gln	Gln	His	Thr	Glu	Asp	Gly	Ser	Pro	Gln	Ala	His	Ile	65	70	75	80
Arg	Gly	Pro	Thr	Gly	Tyr	Leu	Ala	Leu	Glu	Glu	Glu	Gln	Gln	Pro	Ser	85	90	95	
Gln	Gln	Gln	Ala	Ala	Ser	Glu	Gly	His	Pro	Glu	Ser	Ser	Cys	Leu	Pro	100	105	110	
Glu	Pro	Gly	Ala	Ala	Thr	Ala	Pro	Gly	Lys	Gly	Leu	Pro	Gln	Gln	Pro	115	120	125	
Pro	Ala	Pro	Pro	Asp	Gln	Asp	Asp	Ser	Ala	Ala	Pro	Ser	Thr	Leu	Ser	130	135	140	
Leu	Leu	Gly	Pro	Thr	Phe	Pro	Gly	Leu	Ser	Ser	Cys	Ser	Ala	Asp	Ile	145	150	155	160
Lys	Asp	Ile	Leu	Asn	Glu	Ala	Gly	Thr	Met	Gln	Leu	Leu	Gln	Gln	Gln	165	170	175	
Gln	Gln	Gln	Gln	Gln	His	Gln	Gln	Gln	His	Gln	Gln	His	Gln	Gln	Gln	180	185	190	
Gln	Glu	Val	Ile	Ser	Glu	Gly	Ser	Ser	Ala	Arg	Ala	Arg	Glu	Ala	Thr	195	200	205	
Gly	Ala	Pro	Ser	Ser	Ser	Lys	Asp	Ser	Tyr	Leu	Gly	Gly	Asn	Ser	Thr	210	215	220	
Ile	Ser	Asp	Ser	Ala	Lys	Glu	Leu	Cys	Lys	Ala	Val	Ser	Val	Ser	Met	225	230	235	240
Gly	Leu	Gly	Val	Glu	Ala	Leu	Glu	His	Leu	Ser	Pro	Gly	Glu	Gln	Leu	245	250	255	
Arg	Gly	Asp	Cys	Met	Tyr	Ala	Ser	Leu	Leu	Gly	Gly	Pro	Pro	Ala	Val	260	265	270	
Arg	Pro	Thr	Pro	Cys	Ala	Pro	Leu	Pro	Glu	Cys	Lys	Gly	Leu	Pro	Leu	275	280	285	
Asp	Glu	Gly	Pro	Gly	Lys	Ser	Thr	Glu	Glu	Thr	Ala	Glu	Tyr	Ser	Ser	290	295	300	
Phe	Lys	Gly	Gly	Tyr	Ala	Lys	Gly	Leu	Glu	Gly	Glu	Ser	Leu	Gly	Cys	305	310	315	320
Ser	Gly	Ser	Ser	Glu	Ala	Gly	Ser	Ser	Gly	Thr	Leu	Glu	Ile	Pro	Ser	325	330	335	
Ser	Leu	Ser	Leu	Tyr	Lys	Ser	Gly	Ala	Leu	Asp	Glu	Ala	Ala	Ala	Tyr	340	345	350	
Gln	Asn	Arg	Asp	Tyr	Tyr	Asn	Phe	Pro	Leu	Ala	Leu	Ser	Gly	Pro	Pro	355	360	365	
His	Pro	Pro	Pro	Pro	Thr	His	Pro	His	Ala	Arg	Ile	Lys	Leu	Glu	Asn	370	375	380	
Pro	Leu	Asp	Tyr	Gly	Ser	Ala	Trp	Ala	Ala	Ala	Ala	Ala	Gln	Cys	Arg	385	390	395	400
Tyr	Gly	Asp	Leu	Gly	Ser	Leu	His	Gly	Gly	Ser	Val	Ala	Gly	Pro	Ser	405	410	415	
Thr	Gly	Ser	Pro	Pro	Ala	Thr	Thr	Ser	Ser	Ser	Trp	His	Thr	Leu	Phe	420	425	430	
Thr	Ala	Glu	Glu	Gly	Gln	Leu	Tyr	Gly	Pro	Gly	Gly	Gly	Gly	Gly	Ser	435	440	445	
Ser	Ser	Pro	Ser	Asp	Ala	Gly	Pro	Val	Ala	Pro	Tyr	Gly	Tyr	Thr	Arg	450	455	460	
Pro	Pro	Gln	Gly	Leu	Thr	Ser	Gln	Glu	Ser	Asp	Tyr	Ser	Ala	Ser	Glu	465	470	475	480
Val	Trp	Tyr	Pro	Gly	Gly	Val	Val	Asn	Arg	Val	Pro	Tyr	Pro	Ser	Pro	485	490	495	
Asn	Cys	Val	Lys	Ser	Glu	Met	Gly	Pro	Trp	Met	Glu	Asn	Tyr	Ser	Gly	500	505	510	
Pro	Tyr	Gly	Asp	Met	Arg	Leu	Asp	Ser	Thr	Arg	Asp	His	Val	Leu	Pro	515	520	525	
Ile	Asp	Tyr	Tyr	Phe	Pro	Pro	Gln	Lys	Thr	Cys	Leu	Ile	Cys	Gly	Asp	530	535	540	

Glu	Ala	Ser	Gly	Cys	His	Tyr	Gly	Ala	Leu	Thr	Cys	Gly	Ser	Cys	Lys
545					550					555					560
Val	Phe	Phe	Lys	Arg	Ala	Ala	Glu	Gly	Lys	Gln	Lys	Tyr	Leu	Cys	Ala
				565					570					575	
Ser	Arg	Asn	Asp	Cys	Thr	Ile	Asp	Lys	Phe	Arg	Arg	Lys	Asn	Cys	Pro
			580					585					590		
Ser	Cys	Arg	Leu	Arg	Lys	Cys	Tyr	Glu	Ala	Gly	Met	Thr	Leu	Gly	Ala
		595					600					605			
Arg	Lys	Leu	Lys	Lys	Leu	Gly	Asn	Leu	Lys	Leu	Gln	Glu	Glu	Gly	Glu
	610					615					620				
Asn	Ser	Asn	Ala	Gly	Ser	Pro	Thr	Glu	Asp	Pro	Ser	Gln	Lys	Met	Thr
625				630					635						640
Val	Ser	His	Ile	Glu	Gly	Tyr	Glu	Cys	Gln	Pro	Ile	Phe	Leu	Asn	Val
			645						650					655	
Leu	Glu	Ala	Ile	Glu	Pro	Gly	Val	Val	Cys	Ala	Gly	His	Asp	Asn	Asn
		660						665					670		
Gln	Pro	Asp	Ser	Phe	Ala	Ala	Leu	Leu	Ser	Ser	Leu	Asn	Glu	Leu	Gly
		675					680					685			
Glu	Arg	Gln	Leu	Val	His	Val	Val	Lys	Trp	Ala	Lys	Ala	Leu	Pro	Gly
	690					695					700				
Phe	Arg	Asn	Leu	His	Val	Asp	Asp	Gln	Met	Ala	Val	Ile	Gln	Tyr	Ser
705				710					715						720
Trp	Met	Gly	Leu	Met	Val	Phe	Ala	Met	Gly	Trp	Arg	Ser	Phe	Thr	Asn
			725						730				735		
Val	Asn	Ser	Arg	Met	Leu	Tyr	Phe	Ala	Pro	Asp	Leu	Val	Phe	Asn	Glu
		740						745					750		
Tyr	Arg	Met	His	Lys	Ser	Arg	Met	Tyr	Ser	Gln	Cys	Val	Arg	Met	Arg
		755					760					765			
His	Leu	Ser	Gln	Glu	Phe	Gly	Trp	Leu	Gln	Ile	Thr	Pro	Gln	Glu	Phe
	770					775					780				
Leu	Cys	Met	Lys	Ala	Leu	Leu	Leu	Phe	Ser	Ile	Ile	Pro	Val	Asp	Gly
785				790					795					800	
Leu	Lys	Asn	Gln	Lys	Phe	Phe	Asp	Glu	Leu	Arg	Met	Asn	Tyr	Ile	Lys
			805						810					815	
Glu	Leu	Asp	Arg	Ile	Ile	Ala	Cys	Lys	Arg	Lys	Asn	Pro	Thr	Ser	Cys
		820						825					830		
Ser	Arg	Arg	Phe	Tyr	Gln	Leu	Thr	Lys	Leu	Leu	Asp	Ser	Val	Gln	Pro
		835					840					845			
Ile	Ala	Arg	Glu	Leu	His	Gln	Phe	Thr	Phe	Asp	Leu	Leu	Ile	Lys	Ser
	850					855					860				
His	Met	Val	Ser	Val	Asp	Phe	Pro	Glu	Met	Met	Ala	Glu	Ile	Ile	Ser
865				870					875						880
Val	Gln	Val	Pro	Lys	Ile	Leu	Ser	Gly	Lys	Val	Lys	Pro	Ile	Tyr	Phe
			885						890					895	
His	Thr	Gln													

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<210> 17
<211> 2988
<212> DNA
<213> Artificial Sequence
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<220>
<223> Description of Artificial Sequence; note =
        synthetic construct
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<400>	17						
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atggagggtgc	agttagggct	gggaagggtc	taccacgggc	ccccaccaa	gacctatcga		180
ggaqgcqtcc	agaatctgtt	ccagagcggtg	cgcgaagcga	tccagaaccc	gggccccagg		240

caccctgagg	ccgctaacat	agcacctccc	ggcgccctgtt	tacagcagag	gcaggagact	300
agcccccggc	ggcgggcggcg	gcagcagcac	actgaggatg	gttctcctca	agccccacatc	360
agaggcccca	caggctacct	ggccctggag	gaggaacagc	agccttcaca	gcagcaggca	420
gcctccgagg	gccaccctga	gagcagctgc	ctccccgagc	ctggggcggc	caccgctcct	480
ggcaaggggc	tgccgcagca	gccaccagct	cctccagatc	aggatgactc	agctgccccca	540
tccacgttgt	ccctgctggg	ccccactttc	ccaggcttaa	gcagctgctc	cgccgacatt	600
aaagacattt	tgaacgaggc	cggcaccatg	caacttcttc	agcagcagca	acaacagcag	660
cagcaccaac	agcagcacca	acagcaccaa	cagcagcagg	aggtaatctc	cgaaggcagc	720
agcgcaagag	ccaggggaggc	cacgggggct	ccctcttctc	ccaaggatag	ttacctaggg	780
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cccgaatgca	aaggctcttc	cctggacgaa	ggcccaggca	aaagcactga	agagactgct	1020
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tctggcagca	gtgaagcagg	tagctctggg	acacttgaga	tcccgtcctc	tctgtctctg	1140
tataaatctg	gagcactaga	cgaggcagca	gcataccaga	atcgcgacta	ctacaacttt	1200
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tatggggact	tgggtagtct	acatggaggg	agtgtagccg	ggcccagcac	tggatcgccc	1380
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gtatcacaca	ttgaaggcta	tgaatgtcag	cctatctttc	ttaacgtcct	ggaagccatt	2100
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atgctctact	ttgcacctga	cttgggtttc	aatgagtacc	gcattgcaca	gtctcggatg	2400
tccagccagt	gtgtgaggat	gaggcacctg	tctcaagagt	ttggatggct	caaataacc	2460
ccccaggaat	tctgtgcat	gaaagcactg	ctgctcttca	gcattattcc	agtggatggg	2520
ctgaaaaatc	aaaaattctt	tgatgaactt	cgaatgaact	acatcaagga	actcgatcgc	2580
atcattgcat	gcaaaaagaaa	gaatccca	tctgtctcaa	ggcgcttcta	ccagctcacc	2640
aaagctcctg	attctgtgca	gcctatttga	agagagctgc	atcagttcac	ttttgacctg	2700
ctaatacagt	cccatatggt	gagcgtggac	tttctgaaa	tgatggcaga	gatcatctct	2760
gtgcaagtgc	ccaagatcct	ttctgggaaa	gtcaagccca	tctatttcca	cacacagtga	2820
agattttggaa	accctaatac	ccaaaacca	ccttgttccc	tttccagatg	tcttctgcct	2880
gttatataac	tctgcactac	ttctctgcag	tgccttgggg	gaaattcctc	tactgatgta	2940
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<210> 18

<211> 899

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence; note =
synthetic construct

<400> 18

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Lys	Thr	Tyr	Arg	Gly	Ala	Phe	Gln	Asn	Leu	Phe	Gln	Ser	Val	Arg	Glu
			20					25						30	

Ala	Ile	Gln	Asn	Pro	Gly	Pro	Arg	His	Pro	Glu	Ala	Ala	Asn	Ile	Ala
	35						40					45			
Pro	Pro	Gly	Ala	Cys	Leu	Gln	Gln	Arg	Gln	Glu	Thr	Ser	Pro	Arg	Arg
	50					55					60				
Arg	Arg	Arg	Gln	Gln	His	Thr	Glu	Asp	Gly	Ser	Pro	Gln	Ala	His	Ile
65					70					75				80	
Arg	Gly	Pro	Thr	Gly	Tyr	Leu	Ala	Leu	Glu	Glu	Glu	Gln	Gln	Pro	Ser
				85					90					95	
Gln	Gln	Gln	Ala	Ala	Ser	Glu	Gly	His	Pro	Glu	Ser	Ser	Cys	Leu	Pro
			100					105					110		
Glu	Pro	Gly	Ala	Ala	Thr	Ala	Pro	Gly	Lys	Gly	Leu	Pro	Gln	Gln	Pro
		115					120					125			
Pro	Ala	Pro	Pro	Asp	Gln	Asp	Asp	Ser	Ala	Ala	Pro	Ser	Thr	Leu	Ser
	130					135					140				
Leu	Leu	Gly	Pro	Thr	Phe	Pro	Gly	Leu	Ser	Ser	Cys	Ser	Ala	Asp	Ile
145					150					155				160	
Lys	Asp	Ile	Leu	Asn	Glu	Ala	Gly	Thr	Met	Gln	Leu	Leu	Gln	Gln	Gln
				165				170						175	
Gln	Gln	Gln	Gln	Gln	His	Gln	Gln	Gln	His	Gln	Gln	His	Gln	Gln	Gln
			180					185					190		
Gln	Glu	Val	Ile	Ser	Glu	Gly	Ser	Ser	Ala	Arg	Ala	Arg	Glu	Ala	Thr
		195					200					205			
Gly	Ala	Pro	Ser	Ser	Ser	Lys	Asp	Ser	Tyr	Leu	Gly	Gly	Asn	Ser	Thr
	210					215					220				
Ile	Ser	Asp	Ser	Ala	Lys	Glu	Leu	Cys	Lys	Ala	Val	Ser	Val	Ser	Met
225					230					235				240	
Gly	Leu	Gly	Val	Glu	Ala	Leu	Glu	His	Leu	Ser	Pro	Gly	Glu	Gln	Leu
				245				250						255	
Arg	Gly	Asp	Cys	Met	Tyr	Ala	Ser	Leu	Gly	Gly	Pro	Pro	Ala	Val	
			260				265						270		
Arg	Pro	Thr	Pro	Cys	Ala	Pro	Leu	Pro	Glu	Cys	Lys	Gly	Leu	Pro	Leu
		275					280					285			
Asp	Glu	Gly	Pro	Gly	Lys	Ser	Thr	Glu	Glu	Thr	Ala	Glu	Tyr	Ser	Ser
	290					295					300				
Phe	Lys	Gly	Gly	Tyr	Ala	Lys	Gly	Leu	Glu	Gly	Glu	Ser	Leu	Gly	Cys
305					310					315				320	
Ser	Gly	Ser	Ser	Glu	Ala	Gly	Ser	Ser	Gly	Thr	Leu	Glu	Ile	Pro	Ser
				325				330						335	
Ser	Leu	Ser	Leu	Tyr	Lys	Ser	Gly	Ala	Leu	Asp	Glu	Ala	Ala	Ala	Tyr
			340				345						350		
Gln	Asn	Arg	Asp	Tyr	Tyr	Asn	Phe	Pro	Leu	Ala	Leu	Ser	Gly	Pro	Pro
		355					360					365			
His	Pro	Pro	Pro	Pro	Thr	His	Pro	His	Ala	Arg	Ile	Lys	Leu	Glu	Asn
	370					375					380				
Pro	Leu	Asp	Tyr	Gly	Ser	Ala	Trp	Ala	Ala	Ala	Ala	Gln	Cys	Arg	
385					390					395				400	
Tyr	Gly	Asp	Leu	Gly	Ser	Leu	His	Gly	Gly	Ser	Val	Ala	Gly	Pro	Ser
				405				410						415	
Thr	Gly	Ser	Pro	Pro	Ala	Thr	Thr	Ser	Ser	Ser	Trp	His	Thr	Leu	Phe
			420					425					430		
Thr	Ala	Glu	Glu	Gly	Gln	Leu	Tyr	Gly	Pro	Gly	Gly	Gly	Gly	Gly	Ser
			435					440				445			
Ser	Ser	Pro	Ser	Asp	Ala	Gly	Pro	Val	Ala	Pro	Tyr	Gly	Tyr	Thr	Arg
	450					455					460				
Pro	Pro	Gln	Gly	Leu	Thr	Ser	Gln	Glu	Ser	Asp	Tyr	Ser	Ala	Ser	Glu
465					470					475				480	
Val	Trp	Tyr	Pro	Gly	Gly	Val	Val	Asn	Arg	Val	Pro	Tyr	Pro	Ser	Pro
				485				490						495	
Asn	Cys	Val	Lys	Ser	Glu	Met	Gly	Pro	Trp	Met	Glu	Asn	Tyr	Ser	Gly
			500					505					510		

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Pro Tyr Gly Asp Met Arg Leu Asp Ser Thr Arg Asp His Val Leu Pro
    515                      520                      525
Ile Asp Tyr Tyr Phe Pro Pro Gln Lys Thr Cys Leu Ile Cys Gly Asp
    530                      535                      540
Glu Ala Ser Gly Cys His Tyr Gly Ala Leu Thr Cys Gly Ser Cys Lys
545                      550                      555                      560
Val Phe Phe Lys Arg Ala Ala Glu Gly Lys Gln Lys Tyr Leu Cys Ala
    565                      570                      575
Ser Arg Asn Asp Cys Thr Ile Asp Lys Phe Arg Arg Lys Asn Cys Pro
    580                      585                      590
Ser Cys Arg Leu Arg Lys Cys Tyr Glu Ala Gly Met Thr Leu Gly Ala
    595                      600                      605
Arg Lys Leu Lys Lys Leu Gly Asn Leu Lys Leu Gln Glu Glu Gly Glu
    610                      615                      620
Asn Ser Asn Ala Gly Ser Pro Thr Glu Asp Pro Ser Gln Lys Met Thr
625                      630                      635                      640
Val Ser His Ile Glu Gly Tyr Glu Cys Gln Pro Ile Phe Leu Asn Val
    645                      650                      655
Leu Glu Ala Ile Glu Pro Gly Val Val Cys Ala Gly His Asp Asn Asn
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Gln Pro Asp Ser Phe Ala Ala Leu Leu Ser Ser Leu Asn Glu Leu Gly
    675                      680                      685
Glu Arg Gln Leu Val His Val Val Lys Trp Ala Lys Ala Leu Pro Gly
    690                      695                      700
Phe Arg Asn Leu His Val Asp Asp Gln Met Ala Val Ile Gln Tyr Ser
705                      710                      715                      720
Trp Met Gly Leu Met Val Phe Ala Met Gly Trp Arg Ser Phe Thr Asn
    725                      730                      735
Val Asn Ser Arg Met Leu Tyr Phe Ala Pro Asp Leu Val Phe Asn Glu
    740                      745                      750
Tyr Arg Met His Lys Ser Arg Met Tyr Ser Gln Cys Val Arg Met Arg
    755                      760                      765
His Leu Ser Gln Glu Phe Gly Trp Leu Gln Ile Thr Pro Gln Glu Phe
    770                      775                      780
Leu Cys Met Lys Ala Leu Leu Leu Phe Ser Ile Ile Pro Val Asp Gly
785                      790                      795                      800
Leu Lys Asn Gln Lys Phe Phe Asp Glu Leu Arg Met Asn Tyr Ile Lys
    805                      810                      815
Glu Leu Asp Arg Ile Ile Ala Cys Lys Arg Lys Asn Pro Thr Ser Cys
    820                      825                      830
Ser Arg Arg Phe Tyr Gln Leu Thr Lys Leu Leu Asp Ser Val Gln Pro
    835                      840                      845
Ile Ala Arg Glu Leu His Gln Phe Thr Phe Asp Leu Leu Ile Lys Ser
    850                      855                      860
His Met Val Ser Val Asp Phe Pro Glu Met Met Ala Glu Ile Ile Ser
865                      870                      875                      880
Val Gln Val Pro Lys Ile Leu Ser Gly Lys Val Lys Pro Ile Tyr Phe
    885                      890                      895
His Thr Gln

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<210> 19

<211> 2988

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence; note =
synthetic construct

<400> 19

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atggaggtgc	agttagggct	gggaagggtc	taccacaggc	ccccatccaa	gacctatcga	180
ggagcgttcc	agaatctgtt	ccagagcgtg	cggaagcgga	tccagaaccc	gggccccagg	240
caccttgagg	ccgctaacat	agcacctccc	ggcgctgtt	tacagcagag	gcaggagact	300
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agaggcccca	caggctacct	ggccctggag	gaggaacagc	agccttcaca	gcagcaggca	420
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cagcaccaac	agcagcacca	acagcaccaa	cagcagcagg	aggtaatctc	cgaaggcagc	720
agcgcaagag	ccagggaggc	cacgggggct	cctcttctct	ccaaggatag	ttacctaggg	780
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gagtattcct	ctttcaaggg	aggttacgcc	aaaggattgg	aaggtgagag	cttgggggtgc	1080
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gttatataac	tctgcactac	ttctctgcag	tgcttggggg	gaaattcctc	tactgatgta	2940
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<210> 20

<211> 899

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence; note =
synthetic construct

<400> 20

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Lys	Thr	Tyr	Arg	Gly	Ala	Phe	Gln	Asn	Leu	Phe	Gln	Ser	Val	Arg	Glu
			20					25					30		
Ala	Ile	Gln	Asn	Pro	Gly	Pro	Arg	His	Pro	Glu	Ala	Ala	Asn	Ile	Ala
		35					40					45			
Pro	Pro	Gly	Ala	Cys	Leu	Gln	Gln	Arg	Gln	Glu	Thr	Ser	Pro	Arg	Arg
	50					55					60				
Arg	Arg	Arg	Gln	Gln	His	Thr	Glu	Asp	Gly	Ser	Pro	Gln	Ala	His	Ile
65					70					75					80
Arg	Gly	Pro	Thr	Gly	Tyr	Leu	Ala	Leu	Glu	Glu	Gln	Gln	Pro	Ser	
				85					90					95	
Gln	Gln	Gln	Ala	Ala	Ser	Glu	Gly	His	Pro	Glu	Ser	Ser	Cys	Leu	Pro
			100					105					110		
Glu	Pro	Gly	Ala	Ala	Thr	Ala	Pro	Gly	Lys	Gly	Leu	Pro	Gln	Gln	Pro
		115					120						125		
Pro	Ala	Pro	Pro	Asp	Gln	Asp	Asp	Ser	Ala	Ala	Pro	Ser	Thr	Leu	Ser
	130					135					140				
Leu	Leu	Gly	Pro	Thr	Phe	Pro	Gly	Leu	Ser	Ser	Cys	Ser	Ala	Asp	Ile
145					150					155					160
Lys	Asp	Ile	Leu	Asn	Glu	Ala	Gly	Thr	Met	Gln	Leu	Leu	Gln	Gln	Gln
				165					170					175	
Gln	Gln	Gln	Gln	Gln	His	Gln	Gln	Gln	His	Gln	Gln	His	Gln	Gln	Gln
			180					185					190		
Gln	Glu	Val	Ile	Ser	Glu	Gly	Ser	Ser	Ala	Arg	Ala	Arg	Glu	Ala	Thr
		195					200						205		
Gly	Ala	Pro	Ser	Ser	Ser	Lys	Asp	Ser	Tyr	Leu	Gly	Gly	Asn	Ser	Thr
	210					215					220				
Ile	Ser	Asp	Ser	Ala	Lys	Glu	Leu	Cys	Lys	Ala	Val	Ser	Val	Ser	Met
225					230					235					240
Gly	Leu	Gly	Val	Glu	Ala	Leu	Glu	His	Leu	Ser	Pro	Gly	Glu	Gln	Leu
				245					250					255	
Arg	Gly	Asp	Cys	Met	Tyr	Ala	Ser	Leu	Leu	Gly	Gly	Pro	Pro	Ala	Val
			260					265					270		
Arg	Pro	Thr	Pro	Cys	Ala	Pro	Leu	Pro	Glu	Cys	Lys	Gly	Leu	Pro	Leu
		275					280						285		
Asp	Glu	Gly	Pro	Gly	Lys	Ser	Thr	Glu	Glu	Thr	Ala	Glu	Tyr	Ser	Ser
	290					295					300				
Phe	Lys	Gly	Gly	Tyr	Ala	Lys	Gly	Leu	Glu	Gly	Glu	Ser	Leu	Gly	Cys
305					310					315					320
Ser	Gly	Ser	Ser	Glu	Ala	Gly	Ser	Ser	Gly	Thr	Leu	Glu	Ile	Pro	Ser
				325					330					335	
Ser	Leu	Ser	Leu	Tyr	Lys	Ser	Gly	Ala	Leu	Asp	Glu	Ala	Ala	Ala	Tyr
			340					345					350		
Gln	Asn	Arg	Asp	Tyr	Tyr	Asn	Phe	Pro	Leu	Ala	Leu	Ser	Gly	Pro	Pro
	355						360						365		
His	Pro	Pro	Pro	Pro	Thr	His	Pro	His	Ala	Arg	Ile	Lys	Leu	Glu	Asn
	370					375						380			
Pro	Leu	Asp	Tyr	Gly	Ser	Ala	Trp	Ala	Ala	Ala	Ala	Ala	Gln	Cys	Arg
385					390					395					400
Tyr	Gly	Asp	Leu	Gly	Ser	Leu	His	Gly	Gly	Ser	Val	Ala	Gly	Pro	Ser
				405					410					415	
Thr	Gly	Ser	Pro	Pro	Ala	Thr	Thr	Ser	Ser	Ser	Trp	His	Thr	Leu	Phe
			420					425					430		
Thr	Ala	Glu	Gly	Gln	Leu	Tyr	Gly	Pro	Gly	Gly	Gly	Gly	Gly	Gly	Ser
		435					440					445			
Ser	Ser	Pro	Ser	Asp	Ala	Gly	Pro	Val	Ala	Pro	Tyr	Gly	Tyr	Thr	Arg
	450					455					460				
Pro	Pro	Gln	Gly	Leu	Thr	Ser	Gln	Glu	Ser	Asp	Tyr	Ser	Ala	Ser	Glu
465						470				475					480

Val	Trp	Tyr	Pro	Gly	Gly	Val	Val	Asn	Arg	Val	Pro	Tyr	Pro	Ser	Pro	485	490	495
Asn	Cys	Val	Lys	Ser	Glu	Met	Gly	Pro	Trp	Met	Glu	Asn	Tyr	Ser	Gly	500	505	510
Pro	Tyr	Gly	Asp	Met	Arg	Leu	Asp	Ser	Thr	Arg	Asp	His	Val	Leu	Pro	515	520	525
Ile	Asp	Tyr	Tyr	Phe	Pro	Pro	Gln	Lys	Thr	Cys	Leu	Ile	Cys	Gly	Asp	530	535	540
Glu	Ala	Ser	Gly	Cys	His	Tyr	Gly	Ala	Leu	Thr	Cys	Gly	Ser	Cys	Lys	545	550	555
Val	Phe	Phe	Lys	Arg	Ala	Ala	Glu	Gly	Lys	Gln	Lys	Tyr	Leu	Cys	Ala	565	570	575
Ser	Arg	Asn	Asp	Cys	Thr	Ile	Asp	Lys	Phe	Arg	Arg	Lys	Asn	Cys	Pro	580	585	590
Ser	Cys	Arg	Leu	Arg	Lys	Cys	Tyr	Glu	Ala	Gly	Met	Thr	Leu	Gly	Ala	595	600	605
Arg	Lys	Leu	Lys	Lys	Leu	Gly	Asn	Leu	Lys	Leu	Gln	Glu	Glu	Gly	Glu	610	615	620
Asn	Ser	Asn	Ala	Gly	Ser	Pro	Thr	Glu	Asp	Pro	Ser	Gln	Lys	Met	Thr	625	630	635
Val	Ser	His	Ile	Glu	Gly	Tyr	Glu	Cys	Gln	Pro	Ile	Phe	Leu	Asn	Val	645	650	655
Leu	Glu	Ala	Ile	Glu	Pro	Gly	Val	Val	Cys	Ala	Gly	His	Asp	Asn	Asn	660	665	670
Gln	Pro	Asp	Ser	Phe	Ala	Ala	Leu	Leu	Ser	Ser	Leu	Asn	Glu	Leu	Gly	675	680	685
Glu	Arg	Gln	Leu	Val	His	Val	Val	Lys	Trp	Ala	Lys	Ala	Leu	Pro	Gly	690	695	700
Phe	Arg	Asn	Leu	His	Val	Asp	Asp	Gln	Met	Ala	Val	Ile	Gln	Tyr	Ser	705	710	715
Trp	Met	Gly	Leu	Met	Val	Phe	Ala	Met	Gly	Trp	Arg	Ser	Phe	Thr	Asn	725	730	735
Val	Asn	Ser	Arg	Met	Leu	Tyr	Phe	Ala	Pro	Asp	Leu	Val	Phe	Asn	Glu	740	745	750
Tyr	Arg	Met	His	Lys	Ser	Arg	Met	Tyr	Ser	Gln	Cys	Val	Arg	Met	Arg	755	760	765
His	Leu	Ser	Gln	Glu	Phe	Gly	Trp	Leu	Gln	Ile	Thr	Pro	Gln	Glu	Phe	770	775	780
Leu	Cys	Met	Lys	Ala	Leu	Leu	Leu	Phe	Ser	Ile	Ile	Pro	Val	Asp	Gly	785	790	795
Leu	Lys	Asn	Gln	Lys	Phe	Phe	Asp	Glu	Leu	Arg	Met	Asn	Tyr	Ile	Lys	805	810	815
Glu	Leu	Asp	Arg	Ile	Ile	Ala	Cys	Lys	Arg	Lys	Asn	Pro	Thr	Ser	Cys	820	825	830
Ser	Arg	Arg	Phe	Tyr	Gln	Leu	Thr	Lys	Leu	Leu	Asp	Ser	Val	Gln	Pro	835	840	845
Ile	Ala	Arg	Glu	Leu	His	Gln	Phe	Thr	Phe	Asp	Leu	Leu	Ile	Lys	Ser	850	855	860
His	Met	Val	Ser	Val	Asp	Phe	Pro	Glu	Met	Met	Ala	Glu	Ile	Ile	Ser	865	870	875
Val	Gln	Val	Pro	Lys	Ile	Leu	Ser	Gly	Lys	Val	Lys	Pro	Ile	Tyr	Phe	885	890	895
His	Thr	Gln																

<210> 21

<211> 2700

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence; note =
synthetic construct

<400> 21

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<210> 22

<211> 4321

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence; note =
synthetic construct

<400> 22

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-------------	------------	------------	------------	------------	------------	----

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tgcgagagag ctgcatcagt tcacttttga cctgctaate aagtcacaca tgggtgagcgt 3780
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a

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<210> 23

<211> 919

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence; note =
synthetic construct

<400> 23

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 1          5          10          15
Lys Thr Tyr Arg Gly Ala Phe Gln Asn Leu Phe Gln Ser Val Arg Glu
          20          25          30
Val Ile Gln Asn Pro Gly Pro Arg His Pro Glu Ala Ala Ser Ala Ala
          35          40          45
Pro Pro Gly Ala Ser Leu Leu Leu Gln Gln Gln Gln Gln Gln Gln
          50          55          60
Gln Gln Gln Gln Gln Gln Gln Gln Gln Gln Gln Gln Gln Gln Glu Thr
          65          70          75          80
Ser Pro Arg Gln Gln Gln Gln Gln Gln Gly Glu Asp Gly Ser Pro Gln
          85          90          95
Ala His Arg Arg Gly Pro Thr Gly Tyr Leu Val Leu Asp Glu Glu Gln
          100          105          110
Gln Pro Ser Gln Pro Gln Ser Ala Leu Glu Cys His Pro Glu Arg Gly
          115          120          125
Cys Val Pro Glu Pro Gly Ala Ala Val Ala Ala Ser Lys Gly Leu Pro
          130          135          140
Gln Gln Leu Pro Ala Pro Pro Asp Glu Asp Asp Ser Ala Ala Pro Ser
          145          150          155          160
Thr Leu Ser Leu Leu Gly Pro Thr Phe Pro Gly Leu Ser Ser Cys Ser
          165          170          175
Ala Asp Leu Lys Asp Ile Leu Ser Glu Ala Ser Thr Met Gln Leu Leu
          180          185          190
Gln Gln Gln Gln Gln Glu Ala Val Ser Glu Gly Ser Ser Ser Gly Arg
          195          200          205
Ala Arg Glu Ala Ser Gly Ala Pro Thr Ser Ser Lys Asp Asn Tyr Leu
          210          215          220
Gly Gly Thr Ser Thr Ile Ser Asp Asn Ala Lys Glu Leu Cys Lys Ala
          225          230          235          240
Val Ser Val Ser Met Gly Leu Gly Val Glu Ala Leu Glu His Leu Ser
          245          250          255
Pro Gly Glu Gln Leu Arg Gly Asp Cys Met Tyr Ala Pro Leu Leu Gly
          260          265          270
Val Pro Pro Ala Val Arg Pro Thr Pro Cys Ala Pro Leu Ala Glu Cys
          275          280          285
Lys Gly Ser Leu Leu Asp Asp Ser Ala Gly Lys Ser Thr Glu Asp Thr
          290          295          300

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Ala	Glu	Tyr	Ser	Pro	Phe	Lys	Gly	Gly	Tyr	Thr	Lys	Gly	Leu	Glu	Gly		
305					310					315						320	
Glu	Ser	Leu	Gly	Cys	Ser	Gly	Ser	Ala	Ala	Ala	Gly	Ser	Ser	Gly	Thr		
				325					330						335		
Leu	Glu	Leu	Pro	Ser	Thr	Leu	Ser	Leu	Tyr	Lys	Ser	Gly	Ala	Leu	Asp		
			340					345					350				
Glu	Ala	Ala	Ala	Tyr	Gln	Ser	Arg	Asp	Tyr	Tyr	Asn	Phe	Pro	Leu	Ala		
		355					360					365					
Leu	Ala	Gly	Pro	Pro	Pro	Pro	Pro	Pro	Pro	Pro	His	Pro	His	Ala	Arg		
	370					375					380						
Ile	Lys	Leu	Glu	Asn	Pro	Leu	Asp	Tyr	Gly	Ser	Ala	Trp	Ala	Ala	Ala		
385				390						395						400	
Ala	Ala	Gln	Cys	Arg	Tyr	Gly	Asp	Leu	Ala	Ser	Leu	His	Gly	Ala	Gly		
			405					410						415			
Ala	Ala	Gly	Pro	Gly	Ser	Gly	Ser	Pro	Ser	Ala	Ala	Ala	Ser	Ser	Ser		
			420					425					430				
Trp	His	Thr	Leu	Phe	Thr	Ala	Glu	Glu	Gly	Gln	Leu	Tyr	Gly	Pro	Cys		
		435					440						445				
Gly	Gly	Gly	Gly	Gly	Gly	Gly	Gly	Gly	Gly	Gly	Gly	Gly	Gly	Gly	Gly		
	450					455					460						
Gly	Gly	Gly	Gly	Gly	Gly	Gly	Gly	Glu	Ala	Gly	Ala	Val	Ala	Pro	Tyr		
465					470					475					480		
Gly	Tyr	Thr	Arg	Pro	Pro	Gln	Gly	Leu	Ala	Gly	Gln	Glu	Ser	Asp	Phe		
			485					490						495			
Thr	Ala	Pro	Asp	Val	Trp	Tyr	Pro	Gly	Gly	Met	Val	Ser	Arg	Val	Pro		
		500						505					510				
Tyr	Pro	Ser	Pro	Thr	Cys	Val	Lys	Ser	Glu	Met	Gly	Pro	Trp	Met	Asp		
	515						520					525					
Ser	Tyr	Ser	Gly	Pro	Tyr	Gly	Asp	Met	Arg	Leu	Glu	Thr	Ala	Arg	Asp		
	530					535					540						
His	Val	Leu	Pro	Ile	Asp	Tyr	Tyr	Phe	Pro	Pro	Gln	Lys	Thr	Cys	Leu		
545				550						555					560		
Ile	Cys	Gly	Asp	Glu	Ala	Ser	Gly	Cys	His	Tyr	Gly	Ala	Leu	Thr	Cys		
			565						570					575			
Gly	Ser	Cys	Lys	Val	Phe	Phe	Lys	Arg	Ala	Ala	Glu	Gly	Lys	Gln	Lys		
			580					585					590				
Tyr	Leu	Cys	Ala	Ser	Arg	Asn	Asp	Cys	Thr	Ile	Asp	Lys	Phe	Arg	Arg		
	595						600					605					
Lys	Asn	Cys	Pro	Ser	Cys	Arg	Leu	Arg	Lys	Cys	Tyr	Glu	Ala	Gly	Met		
	610					615						620					
Thr	Leu	Gly	Ala	Arg	Lys	Leu	Lys	Lys	Leu	Gly	Asn	Leu	Lys	Leu	Gln		
625					630						635				640		
Glu	Glu	Gly	Glu	Ala	Ser	Ser	Thr	Thr	Ser	Pro	Thr	Glu	Glu	Thr	Thr		
			645						650					655			
Gln	Lys	Leu	Thr	Val	Ser	His	Ile	Glu	Gly	Tyr	Glu	Cys	Gln	Pro	Ile		
		660						665					670				
Phe	Leu	Asn	Val	Leu	Glu	Ala	Ile	Glu	Pro	Gly	Val	Val	Cys	Ala	Gly		
	675						680					685					
His	Asp	Asn	Asn	Gln	Pro	Asp	Ser	Phe	Ala	Ala	Leu	Leu	Ser	Ser	Leu		
	690					695					700						
Asn	Glu	Leu	Gly	Glu	Arg	Gln	Leu	Val	His	Val	Val	Lys	Trp	Ala	Lys		
705					710					715					720		
Ala	Leu	Pro	Gly	Phe	Arg	Asn	Leu	His	Val	Asp	Asp	Gln	Met	Ala	Val		
			725						730					735			
Ile	Gln	Tyr	Ser	Trp	Met	Gly	Leu	Met	Val	Phe	Ala	Met	Gly	Trp	Arg		
		740						745					750				
Ser	Phe	Thr	Asn	Val	Asn	Ser	Arg	Met	Leu	Tyr	Phe	Ala	Pro	Asp	Leu		
	755						760					765					
Val	Phe	Asn	Glu	Tyr	Arg	Met	His	Lys	Ser	Arg	Met	Tyr	Ser	Gln	Cys		
	770					775						780					

Val	Arg	Met	Arg	His	Leu	Ser	Gln	Glu	Phe	Gly	Trp	Leu	Gln	Ile	Thr	785	790	795	800
Pro	Gln	Glu	Phe	Leu	Cys	Met	Lys	Ala	Leu	Leu	Leu	Phe	Ser	Ile	Ile	805	810	815	
Pro	Val	Asp	Gly	Leu	Lys	Asn	Gln	Lys	Phe	Phe	Asp	Glu	Leu	Arg	Met	820	825	830	
Asn	Tyr	Ile	Lys	Glu	Leu	Asp	Arg	Ile	Ile	Ala	Cys	Lys	Arg	Lys	Asn	835	840	845	
Pro	Thr	Ser	Cys	Ser	Arg	Arg	Phe	Tyr	Gln	Leu	Thr	Lys	Leu	Leu	Asp	850	855	860	
Ser	Val	Gln	Pro	Ile	Ala	Arg	Glu	Leu	His	Gln	Phe	Thr	Phe	Asp	Leu	865	870	875	880
Leu	Ile	Lys	Ser	His	Met	Val	Ser	Val	Asp	Phe	Pro	Glu	Met	Met	Ala	885	890	895	
Glu	Ile	Ile	Ser	Val	Gln	Val	Pro	Lys	Ile	Leu	Ser	Gly	Lys	Val	Lys	900	905	910	
Pro	Ile	Tyr	Phe	His	Thr	Gln										915			

<210> 24

<211> 595

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence; note =
synthetic construct

<400> 24

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Ile	Pro	Leu	Glu	Arg	Pro	Leu	Gly	Glu	Val	Tyr	Leu	Asp	Ser	Ser	Lys	35	40	45	
Pro	Ala	Val	Tyr	Asn	Tyr	Pro	Glu	Gly	Ala	Ala	Tyr	Glu	Phe	Asn	Ala	50	55	60	
Ala	Ala	Ala	Ala	Asn	Ala	Gln	Val	Tyr	Gly	Gln	Thr	Gly	Leu	Pro	Tyr	65	70	75	80
Gly	Pro	Gly	Ser	Glu	Ala	Ala	Ala	Phe	Gly	Ser	Asn	Gly	Leu	Gly	Gly	85	90	95	
Phe	Pro	Pro	Leu	Asn	Ser	Val	Ser	Pro	Ser	Pro	Leu	Met	Leu	Leu	His	100	105	110	
Pro	Pro	Pro	Gln	Leu	Ser	Pro	Phe	Leu	Gln	Pro	His	Gly	Gln	Gln	Val	115	120	125	
Pro	Tyr	Tyr	Leu	Glu	Asn	Glu	Pro	Ser	Gly	Tyr	Thr	Val	Arg	Glu	Ala	130	135	140	
Gly	Pro	Pro	Ala	Phe	Tyr	Arg	Pro	Asn	Ser	Asp	Asn	Arg	Arg	Gln	Gly	145	150	155	160
Gly	Arg	Glu	Arg	Leu	Ala	Ser	Thr	Asn	Asp	Lys	Gly	Ser	Met	Ala	Met	165	170	175	
Glu	Ser	Ala	Lys	Glu	Thr	Arg	Tyr	Cys	Ala	Val	Cys	Asn	Asp	Tyr	Ala	180	185	190	
Ser	Gly	Tyr	His	Tyr	Gly	Val	Trp	Ser	Cys	Glu	Gly	Cys	Lys	Ala	Phe	195	200	205	
Phe	Lys	Arg	Ser	Ile	Gln	Gly	His	Asn	Asp	Tyr	Met	Cys	Pro	Ala	Thr	210	215	220	
Asn	Gln	Cys	Thr	Ile	Asp	Lys	Asn	Arg	Arg	Lys	Ser	Cys	Gln	Ala	Cys	225	230	235	240
Arg	Leu	Arg	Lys	Cys	Tyr	Glu	Val	Gly	Met	Met	Lys	Gly	Gly	Ile	Arg	245	250	255	

Lys Asp Arg Arg Gly Gly Arg Met Leu Lys His Lys Arg Gln Arg Asp
260 265 270
Asp Gly Glu Gly Arg Gly Glu Val Gly Ser Ala Gly Asp Met Arg Ala
275 280 285
Ala Asn Leu Trp Pro Ser Pro Leu Met Ile Lys Arg Ser Lys Lys Asn
290 295 300
Ser Leu Ala Leu Ser Leu Thr Ala Asp Gln Met Val Ser Ala Leu Leu
305 310 315 320
Asp Ala Glu Pro Pro Ile Leu Tyr Ser Glu Tyr Asp Pro Thr Arg Pro
325 330 335
Phe Ser Glu Ala Ser Met Met Gly Leu Leu Thr Asn Leu Ala Asp Arg
340 345 350
Glu Leu Val His Met Ile Asn Trp Ala Lys Arg Val Pro Gly Phe Val
355 360 365
Asp Leu Thr Leu His Asp Gln Val His Leu Leu Glu Cys Ala Trp Leu
370 375 380
Glu Ile Leu Met Ile Gly Leu Val Trp Arg Ser Met Glu His Pro Val
385 390 395 400
Lys Leu Leu Phe Ala Pro Asn Leu Leu Leu Asp Arg Asn Gln Gly Lys
405 410 415
Cys Val Glu Gly Met Val Glu Ile Phe Asp Met Leu Leu Ala Thr Ser
420 425 430
Ser Arg Phe Arg Met Met Asn Leu Gln Gly Glu Glu Phe Val Cys Leu
435 440 445
Lys Ser Ile Ile Leu Leu Asn Ser Gly Val Tyr Thr Phe Leu Ser Ser
450 455 460
Thr Leu Lys Ser Leu Glu Glu Lys Asp His Ile His Arg Val Leu Asp
465 470 475 480
Lys Ile Thr Asp Thr Leu Ile His Leu Met Ala Lys Ala Gly Leu Thr
485 490 495
Leu Gln Gln Gln His Gln Arg Leu Ala Gln Leu Leu Leu Ile Leu Ser
500 505 510
His Ile Arg His Met Ser Asn Lys Gly Met Glu His Leu Tyr Ser Met
515 520 525
Lys Cys Lys Asn Val Val Pro Leu Tyr Asp Leu Leu Leu Glu Met Leu
530 535 540
Asp Ala His Arg Leu His Ala Pro Thr Ser Arg Gly Gly Ala Ser Val
545 550 555 560
Glu Glu Thr Asp Gln Ser His Leu Ala Thr Ala Gly Ser Thr Ser Ser
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His Ser Leu Gln Lys Tyr Tyr Ile Thr Gly Glu Ala Glu Gly Phe Pro
580 585 590
Ala Thr Val
595

<210> 25

<211> 6450

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence; note =
synthetic construct

<400> 25

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gccggcttca	ccggaccgca	ggctcccggg	gcagggccgg	ggccagagct	cgcgtgtcgg	240
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gaggtgtacc	tggacagcag	caagcccgc	gtgtacaact	accccgaggg	cgccgcctac	540
gagttcaacg	ccgcggccgc	cgccaacgcg	caggtctacg	gtcagaccgg	cctccccctac	600
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<210> 26

<211> 614

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence; note =
synthetic construct

<400> 26

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Leu Leu Arg Cys Ser Asp Ala Arg Arg Asp Leu Glu Leu Ala Ile Gly
      20             25             30
Gly Val Leu Arg Ala Glu Gln Gln Ile Lys Asp Asn Leu Arg Glu Val
      35             40             45

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65					70					75					80
Lys	Glu	Glu	Thr	Leu	Gln	Gln	Gln	Ala	Gln	Gln	Leu	Tyr	Ser	Leu	Leu
				85					90					95	
Gly	Gln	Phe	Asn	Cys	Leu	Thr	His	Gln	Leu	Glu	Cys	Thr	Gln	Asn	Lys
			100					105					110		
Asp	Leu	Ala	Asn	Gln	Val	Ser	Val	Cys	Leu	Glu	Arg	Leu	Gly	Ser	Leu
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Thr	Leu	Lys	Pro	Glu	Asp	Ser	Thr	Val	Leu	Leu	Phe	Glu	Ala	Asp	Thr
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Ile	Thr	Leu	Arg	Gln	Thr	Ile	Thr	Thr	Phe	Gly	Ser	Leu	Lys	Thr	Ile
145					150					155					160
Gln	Ile	Pro	Glu	His	Leu	Met	Ala	His	Ala	Ser	Ser	Ala	Asn	Ile	Gly
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Pro	Phe	Leu	Glu	Lys	Arg	Gly	Cys	Ile	Ser	Met	Pro	Glu	Gln	Lys	Ser
	180						185						190		
Ala	Ser	Gly	Ile	Val	Ala	Val	Pro	Phe	Ser	Glu	Trp	Leu	Leu	Gly	Ser
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Lys	Pro	Ala	Ser	Gly	Tyr	Gln	Ala	Pro	Tyr	Ile	Pro	Ser	Thr	Asp	Pro
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Gln	Asp	Trp	Leu	Thr	Gln	Lys	Gln	Thr	Leu	Glu	Asn	Ser	Gln	Thr	Ser
225					230					235					240
Ser	Arg	Ala	Cys	Asn	Phe	Phe	Asn	Asn	Val	Gly	Gly	Asn	Leu	Lys	Gly
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Leu	Glu	Asn	Trp	Leu	Leu	Lys	Ser	Glu	Lys	Ser	Ser	Tyr	Gln	Lys	Cys
		260						265					270		
Asn	Ser	His	Ser	Thr	Thr	Ser	Ser	Phe	Ser	Ile	Glu	Met	Glu	Lys	Val
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Gly	Asp	Gln	Glu	Leu	Pro	Asp	Gln	Asp	Glu	Met	Asp	Leu	Ser	Asp	Trp
	290					295					300				
Leu	Val	Thr	Pro	Gln	Glu	Ser	His	Lys	Leu	Arg	Lys	Pro	Glu	Asn	Gly
305					310					315					320
Ser	Arg	Glu	Thr	Ser	Glu	Lys	Phe	Lys	Leu	Leu	Phe	Gln	Ser	Tyr	Asn
			325						330					335	
Val	Asn	Asp	Trp	Leu	Val	Lys	Thr	Asp	Ser	Cys	Thr	Asn	Cys	Gln	Gly
	340							345					350		
Asn	Gln	Pro	Lys	Gly	Val	Glu	Ile	Glu	Asn	Leu	Gly	Asn	Leu	Lys	Cys
	355						360					365			
Leu	Asn	Asp	His	Leu	Glu	Ala	Lys	Lys	Pro	Leu	Ser	Thr	Pro	Ser	Met
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Val	Thr	Glu	Asp	Trp	Leu	Val	Gln	Asn	His	Gln	Asp	Pro	Cys	Lys	Val
385					390					395					400
Glu	Glu	Val	Cys	Arg	Ala	Asn	Glu	Pro	Cys	Thr	Ser	Phe	Ala	Glu	Cys
			405						410					415	
Val	Cys	Asp	Glu	Asn	Cys	Glu	Lys	Glu	Ala	Leu	Tyr	Lys	Trp	Leu	Leu
		420						425					430		
Lys	Lys	Glu	Gly	Lys	Asp	Lys	Asn	Gly	Met	Pro	Val	Glu	Pro	Lys	Pro
	435						440					445			
Glu	Pro	Glu	Lys	His	Lys	Asp	Ser	Leu	Asn	Met	Trp	Leu	Cys	Pro	Arg
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Lys	Glu	Val	Ile	Glu	Gln	Thr	Lys	Ala	Pro	Lys	Ala	Met	Thr	Pro	Ser
465					470					475					480
Arg	Ile	Ala	Asp	Ser	Phe	Gln	Val	Ile	Lys	Asn	Ser	Pro	Leu	Ser	Glu
			485						490					495	
Trp	Leu	Ile	Arg	Pro	Pro	Tyr	Lys	Glu	Gly	Ser	Pro	Lys	Glu	Val	Pro
		500						505					510		
Gly	Thr	Glu	Asp	Arg	Ala	Gly	Lys	Gln	Lys	Phe	Lys	Ser	Pro	Met	Asn
	515						520					525			

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Thr Ser Trp Cys Ser Phe Asn Thr Ala Asp Trp Val Leu Pro Gly Lys
530                               535                               540
Lys Met Gly Asn Leu Ser Gln Leu Ser Ser Gly Glu Asp Lys Trp Leu
545                               550                               555                               560
Leu Arg Lys Lys Ala Gln Glu Val Leu Leu Asn Ser Pro Leu Gln Glu
565                               570                               575
Glu His Asn Phe Pro Pro Asp His Tyr Gly Leu Pro Ala Val Cys Asp
580                               585                               590
Leu Phe Ala Cys Met Gln Leu Lys Val Asp Lys Glu Lys Trp Leu Tyr
595                               600                               605
Arg Thr Pro Leu Gln Met
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<210> 27
 <211> 1845
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence; note =
 synthetic construct

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<400> 27
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<210> 28
 <211> 474
 <212> PRT
 <213> Artificial Sequence

<220>

Pro Gly Ser Pro Cys Phe Asn Arg Leu Phe Tyr Ala Val Asp Val Asp
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 Asp Asp Ile Trp Glu Asp Glu Val Glu Asp
 465 470

<210> 29
 <211> 1701
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence; note =
 synthetic construct

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<210> 30
 <211> 444
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence; note =
 synthetic construct

<400> 30
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 Pro Pro Pro Ser Tyr Gly His Gln Pro Gln Thr Gly Ser Gly Glu Ser
 20 25 30

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	35						40					45			
Pro	Arg	Ser	Pro	Lys	Pro	Ala	Ala	Pro	Ala	Ala	Pro	Pro	Phe	Ser	Ser
	50					55					60				
Ser	Ser	Gly	Val	Leu	Gly	Thr	Gly	Leu	Cys	Glu	Leu	Asp	Arg	Leu	Leu
65					70					75					80
Gln	Glu	Leu	Asn	Ala	Thr	Gln	Phe	Asn	Ile	Thr	Asp	Glu	Ile	Met	Ser
			85						90					95	
Gln	Phe	Pro	Ser	Ser	Lys	Val	Ala	Ser	Gly	Glu	Gln	Lys	Glu	Asp	Gln
		100						105					110		
Ser	Glu	Asp	Lys	Lys	Arg	Pro	Ser	Leu	Pro	Ser	Ser	Pro	Ser	Pro	Gly
		115					120					125			
Leu	Pro	Lys	Ala	Ser	Ala	Thr	Ser	Ala	Thr	Leu	Glu	Leu	Asp	Arg	Leu
	130					135					140				
Met	Ala	Ser	Leu	Pro	Asp	Phe	Arg	Val	Gln	Asn	His	Leu	Pro	Ala	Ser
145					150					155					160
Gly	Pro	Thr	Gln	Pro	Pro	Val	Val	Ser	Ser	Thr	Asn	Glu	Gly	Ser	Pro
			165					170						175	
Ser	Pro	Pro	Glu	Pro	Thr	Ala	Lys	Gly	Ser	Leu	Asp	Thr	Met	Leu	Gly
		180					185						190		
Leu	Leu	Gln	Ser	Asp	Leu	Ser	Arg	Arg	Gly	Val	Pro	Thr	Gln	Ala	Lys
	195						200					205			
Gly	Leu	Cys	Gly	Ser	Cys	Asn	Lys	Pro	Ile	Ala	Gly	Gln	Val	Val	Thr
	210					215					220				
Ala	Leu	Gly	Arg	Ala	Trp	His	Pro	Glu	His	Phe	Val	Cys	Gly	Gly	Cys
225					230					235					240
Ser	Thr	Ala	Leu	Gly	Gly	Ser	Ser	Phe	Phe	Glu	Lys	Asp	Gly	Ala	Pro
			245					250						255	
Phe	Cys	Pro	Glu	Cys	Tyr	Phe	Glu	Arg	Phe	Ser	Pro	Arg	Cys	Gly	Phe
		260					265						270		
Cys	Asn	Gln	Pro	Ile	Arg	His	Lys	Met	Val	Thr	Ala	Leu	Gly	Thr	His
	275						280					285			
Trp	His	Pro	Glu	His	Phe	Cys	Cys	Val	Ser	Cys	Gly	Glu	Pro	Phe	Gly
	290					295					300				
Asp	Glu	Gly	Phe	His	Glu	Arg	Glu	Gly	Arg	Pro	Tyr	Cys	Arg	Arg	Asp
305					310					315					320
Phe	Leu	Gln	Leu	Phe	Ala	Pro	Arg	Cys	Gln	Gly	Cys	Gln	Gly	Pro	Ile
			325					330						335	
Leu	Asp	Asn	Tyr	Ile	Ser	Ala	Leu	Ser	Leu	Leu	Trp	His	Pro	Asp	Cys
		340					345						350		
Phe	Val	Cys	Arg	Glu	Cys	Phe	Ala	Pro	Phe	Ser	Gly	Gly	Ser	Phe	Phe
		355					360					365			
Glu	His	Glu	Gly	Arg	Pro	Leu	Cys	Glu	Asn	His	Phe	His	Ala	Arg	Arg
	370					375					380				
Gly	Ser	Leu	Trp	Pro	Thr	Cys	Gly	Leu	Pro	Val	Thr	Gly	Arg	Cys	Val
385					390					395					400
Ser	Ala	Leu	Gly	Arg	Arg	Phe	His	Pro	Asp	His	Phe	Ala	Cys	Thr	Phe
			405					410						415	
Cys	Leu	Arg	Pro	Leu	Thr	Lys	Gly	Ser	Phe	Gln	Glu	Arg	Ala	Gly	Lys
		420					425						430		
Pro	Tyr	Cys	Gln	Pro	Cys	Phe	Leu	Lys	Leu	Phe	Gly				
	435						440								

<210> 31

<211> 1335

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence; note =
synthetic construct

<400> 31

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atgccaaaggt cagggggctcc caaagagcgc cctgcggagc ctctcacccc tccccatcc      60

tatggccacc agccacagac aggggtctggg gagtcttcag gagcctcggg ggacaaggac      120
cacctgtaca gcacggtatg caagcctcgg tccccaaagc ctgcagcccc ggccgcccct      180
ccattctcct cttccagcgg tgtcttgggt accgggctct gtgagctaga tcggttgctt      240
caggaactta atgccactca gttcaacatc acagatgaaa tcatgtctca gttcccatct      300
agcaaggtgg cttcaggaga gcagaaggag gaccagtctg aagataagaa aagaccagc      360
ctcccttcca gcccgtctcc tggcctccca aaggcttctg ccacctcagc cactctggag      420
ctggatagac tgatggcctc actccctgac ttccgcgttc aaaaccatct tccagcctct      480
gggccaactc agccaccggt ggtgagctcc acaaatgagg gctcccatc cccaccagag      540
ccgactgcaa agggcagcct agacaccatg ctggggctgc tgcagtccga cctcagccgc      600
cggggtgttc ccaccaggc caaaggcctc tgtggctcct gcaataaacc tattgctggg      660
caagtggatga cggctctggg ccgcgcctgg caccocgagc acttcgtttg cggaggctgt      720
tccaccgccc tgggaggcag cagcttcttc gagaaggatg gagccccctt ctgccccgag      780
tgctactttg agcgttcttc gccaaagatgt ggcttctgca accagcccat ccgacacaag      840
atggtgaccg ccttgggcac tctactggcag ccagagcatt tctgctgcgt cagttgcggg      900
gagcccttcg gagatgaggg tttccacgag cgcgagggcc gccctactg ccgcccggac      960
ttctcgagc tggtcgcccc gcgtgcccag ggctgcccag gcccctactg ggataactac     1020
atctcgcgcc tcagcctgct ctggcaccgg gactgtttcg tctgcaggga atgcttcgcg     1080
cccttctcgg gaggcagcct tttcagacac gagggccgcc cgttgtgcga gaaccacttc     1140
cacgcacgac gcggctcgct gtggcccacg tgtggcctcc ctgtgaccgg ccgctgcgtg     1200
tcggccctgg gtcgcccgtt ccaccgggac cacttcgcat gcaccttctg cctgcgcccg     1260
ctcaccaagg ggtccttcca ggagcgcgcc ggcaagccct actgccagcc ctgcttcctg     1320
aagctcttcg gctga                                     1335

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<210> 32

<211> 216

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence; note =
synthetic construct

<400> 32

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Met Ala Ala Gln Gly Glu Pro Gln Val Gln Phe Lys Leu Val Leu Val
 1              5              10              15
Gly Asp Gly Gly Thr Gly Lys Thr Thr Phe Val Lys Arg His Leu Thr
      20              25              30
Gly Glu Phe Glu Lys Lys Tyr Val Ala Thr Leu Gly Val Glu Val His
      35              40              45
Pro Leu Val Phe His Thr Asn Arg Gly Pro Ile Lys Phe Asn Val Trp
      50              55              60
Asp Thr Ala Gly Gln Glu Lys Phe Gly Gly Leu Arg Asp Gly Tyr Tyr
      65              70              75              80
Ile Gln Ala Gln Cys Ala Ile Ile Met Phe Asp Val Thr Ser Arg Val
      85              90              95
Thr Tyr Lys Asn Val Pro Asn Trp His Arg Asp Leu Val Arg Val Cys
      100             105             110
Glu Asn Ile Pro Ile Val Leu Cys Gly Asn Lys Val Asp Ile Lys Asp
      115             120             125
Arg Lys Val Lys Ala Lys Ser Ile Val Phe His Arg Lys Lys Asn Leu
      130             135             140
Gln Tyr Tyr Asp Ile Ser Ala Lys Ser Asn Tyr Asn Phe Glu Lys Pro
      145             150             155             160
Phe Leu Trp Leu Ala Arg Lys Leu Ile Gly Asp Pro Asn Leu Glu Phe
      165             170             175
Val Ala Met Pro Ala Leu Ala Pro Pro Glu Val Val Met Asp Pro Ala
      180             185             190

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Leu Ala Ala Gln Tyr Glu His Asp Leu Glu Val Ala Gln Thr Thr Ala
 195 200 205
 Leu Pro Asp Glu Asp Asp Asp Leu
 210 215

<210> 33
 <211> 1566
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence; note =
 synthetic construct

<400> 33
 ggcgcttctg gaaggaacgc cgcgatggct ggcgagggag agccccaggt ccagttcaaa 60
 cttgtatttg ttggtgatgg tggtagctga aaaacgacct tcgtgaaacg tcatttgact 120
 ggtgaatttg agaagaagta ttagaccacc ttgggtggtg aggttcatcc cctagtgttc 180
 cacaccaaca gaggacctat taagttcaat gtatgggaca cagccggcca ggagaaattc 240
 ggtggactga gagatggcta ttatatccaa gccagtggtg ccatcataat gtttgatgta 300
 acatcgagag ttactttaca gaatgtgctt aactggcata gagatctggt acgagtgtgt 360
 gaaaacatcc ccattgtgtt gtgtggcaac aaagtggata ttaaggacag gaaagtgaag 420
 gcgaaatcca ttgtcttcca ccgaaagaag aatcttcagt actacgacat ttctgcaaaa 480
 agtaactaca actttgaaaa gcccttcctc tggcttgcta ggaagctcat tggagaccct 540
 aacttggaat ttgttgccat gcctgctctc gcccaccag aagttgtcat ggaccagct 600
 ttggcagcac agtatgagca cgacttagag gttgctcaga caactgctct cccggatgag 660
 gatgatgacc tgtgagaatg aagctggagc ccagcgtcag aagtctagtt ttataggcag 720
 ctgtcctgtg atgtcagcgg tgcagcgtgt gtgccacctc attattatct agctaagcgg 780
 aacatgtgct ttatctgtgg gatgctgaag gagatgagtg ggcttcggag tgaatgtggc 840
 agtttaaaaa ataacttcat tgtttggacc tgcataattta gctgtttgga cgcagttgat 900
 tccttgagtt tcatatataa gactgctgca gtcacatcac aatattcagt ggtgaaatct 960
 tgtttgttac tgtcattccc attccttttc tttagaatca gaataaagtt gtatttcaaa 1020
 tatctaagca agtgaactca tcccttgttt ataaatagca tttggaaacc actaaagtag 1080
 ggaagtttta tgccatgtta atatttgaat tgccttgctt ttatcactta atttgaaatc 1140
 tattgggtta atttctccct atgtttatth ttgtacattt gagccatgtc acacaaactg 1200
 atgatgacag gtcagcagta ttctatttgg ttagaagggt tacatggtgt aaatattagt 1260
 gcagttaagc taaagcagtg tttgctccac ctccatattg gctaggtagg gtcacctagg 1320
 gaagcacttg ctcaaaaatct gtgacctgac agaataaaaa tgtggtttgt acatatcaaa 1380
 tagatattht aagggttaata ttttctttta tggcaaaagt aatcatgttt taatgtagaa 1440
 cctcaaacag gatggaacat cagtggatgg caggaggttg ggaattcttg ctgttaaaaa 1500
 taattacaaa ttttgcaactt tttgtttgaa tgtttagatgc ttagtgtgaa gttgatacgc 1560
 aagccg 1566

<210> 34
 <211> 2427
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence; note =
 synthetic construct

<400> 34
 Met Pro Leu Lys Thr Arg Thr Ala Leu Ser Asp Asp Pro Asp Ser Ser
 1 5 10 15
 Thr Ser Thr Leu Gly Asn Met Leu Glu Leu Pro Gly Thr Ser Ser Ser
 20 25 30
 Ser Thr Ser Gln Glu Leu Pro Phe Cys Gln Pro Lys Lys Lys Ser Thr
 35 40 45
 Pro Leu Lys Tyr Glu Val Gly Asp Leu Ile Trp Ala Lys Phe Lys Arg
 50 55 60

Arg	Pro	Trp	Trp	Pro	Cys	Arg	Ile	Cys	Ser	Asp	Pro	Leu	Ile	Asn	Thr	65	70	75	80
His	Ser	Lys	Met	Lys	Val	Ser	Asn	Arg	Arg	Pro	Tyr	Arg	Gln	Tyr	Tyr	85	90	95	
Val	Glu	Ala	Phe	Gly	Asp	Pro	Ser	Glu	Arg	Ala	Trp	Val	Ala	Gly	Lys	100	105	110	
Ala	Ile	Val	Met	Phe	Glu	Gly	Arg	His	Gln	Phe	Glu	Glu	Leu	Pro	Val	115	120	125	
Leu	Arg	Arg	Arg	Gly	Lys	Gln	Lys	Glu	Lys	Gly	Tyr	Arg	His	Lys	Val	130	135	140	
Pro	Gln	Lys	Ile	Leu	Ser	Lys	Trp	Glu	Ala	Ser	Val	Gly	Leu	Ala	Glu	145	150	155	160
Gln	Tyr	Asp	Val	Pro	Lys	Gly	Ser	Lys	Asn	Arg	Lys	Cys	Ile	Pro	Gly	165	170		175
Ser	Ile	Lys	Leu	Asp	Ser	Glu	Glu	Asp	Met	Pro	Phe	Glu	Asp	Cys	Thr	180	185		190
Asn	Asp	Pro	Glu	Ser	Glu	His	Asp	Leu	Leu	Leu	Asn	Gly	Cys	Leu	Lys	195	200	205	
Ser	Leu	Ala	Phe	Asp	Ser	Glu	His	Ser	Ala	Asp	Glu	Lys	Glu	Lys	Pro	210	215	220	
Cys	Ala	Lys	Ser	Arg	Ala	Arg	Lys	Ser	Ser	Asp	Asn	Pro	Lys	Arg	Thr	225	230	235	240
Ser	Val	Lys	Lys	Gly	His	Ile	Gln	Phe	Glu	Ala	His	Lys	Asp	Glu	Arg	245	250		255
Arg	Gly	Lys	Ile	Pro	Glu	Asn	Leu	Gly	Leu	Asn	Phe	Ile	Ser	Gly	Asp	260	265	270	
Ile	Ser	Asp	Thr	Gln	Ala	Ser	Asn	Glu	Leu	Ser	Arg	Ile	Ala	Asn	Ser				
																275	280	285	
Leu	Thr	Gly	Ser	Asn	Thr	Ala	Pro	Gly	Ser	Phe	Leu	Phe	Ser	Ser	Cys	290	295	300	
Gly	Lys	Asn	Thr	Ala	Lys	Lys	Glu	Phe	Glu	Thr	Ser	Asn	Gly	Asp	Ser	305	310	315	320
Leu	Leu	Gly	Leu	Pro	Glu	Gly	Ala	Leu	Ile	Ser	Lys	Cys	Ser	Arg	Glu	325	330	335	
Lys	Asn	Lys	Pro	Gln	Arg	Ser	Leu	Val	Cys	Gly	Ser	Lys	Val	Lys	Leu	340	345	350	
Cys	Tyr	Ile	Gly	Ala	Gly	Asp	Glu	Lys	Arg	Ser	Asp	Ser	Ile	Ser		355	360	365	
Ile	Cys	Thr	Thr	Ser	Asp	Asp	Gly	Ser	Ser	Asp	Leu	Asp	Pro	Ile	Glu	370	375	380	
His	Ser	Ser	Glu	Ser	Asp	Asn	Ser	Val	Leu	Glu	Ile	Pro	Asp	Ala	Phe	385	390	395	400
Asp	Arg	Thr	Glu	Asn	Met	Leu	Ser	Met	Gln	Lys	Asn	Glu	Lys	Ile	Lys	405	410		415
Tyr	Ser	Arg	Phe	Ala	Ala	Thr	Asn	Thr	Arg	Val	Lys	Ala	Lys	Gln	Lys	420	425	430	
Pro	Leu	Ile	Ser	Asn	Ser	His	Thr	Asp	His	Leu	Met	Gly	Cys	Thr	Lys	435	440	445	
Ser	Ala	Glu	Pro	Gly	Thr	Glu	Thr	Ser	Gln	Val	Asn	Leu	Ser	Asp	Leu	450	455	460	
Lys	Ala	Ser	Thr	Leu	Val	His	Lys	Pro	Gln	Ser	Asp	Phe	Thr	Asn	Asp	465	470	475	480
Ala	Leu	Ser	Pro	Lys	Phe	Asn	Leu	Ser	Ser	Ile	Ser	Ser	Glu	Asn		485	490	495	
Ser	Leu	Ile	Lys	Gly	Gly	Ala	Ala	Asn	Gln	Ala	Leu	Leu	His	Ser	Lys	500	505	510	
Ser	Lys	Gln	Pro	Lys	Phe	Arg	Ser	Ile	Lys	Cys	Lys	His	Lys	Glu	Asn	515	520	525	
Pro	Val	Met	Ala	Glu	Pro	Pro	Val	Ile	Asn	Glu	Glu	Cys	Ser	Leu	Lys	530	535	540	

Cys	Cys	Ser	Ser	Asp	Thr	Lys	Gly	Ser	Pro	Leu	Ala	Ser	Ile	Ser	Lys
545					550					555					560
Ser	Gly	Lys	Val	Asp	Gly	Leu	Lys	Leu	Leu	Asn	Asn	Met	His	Glu	Lys
				565					570					575	
Thr	Arg	Asp	Ser	Ser	Asp	Ile	Glu	Thr	Ala	Val	Val	Lys	His	Val	Leu
			580					585					590		
Ser	Glu	Leu	Lys	Glu	Leu	Ser	Tyr	Arg	Ser	Leu	Gly	Glu	Asp	Val	Ser
	595						600					605			
Asp	Ser	Gly	Thr	Ser	Lys	Pro	Ser	Lys	Pro	Leu	Leu	Phe	Ser	Ser	Ala
	610					615					620				
Ser	Ser	Gln	Asn	His	Ile	Pro	Ile	Glu	Pro	Asp	Tyr	Lys	Phe	Ser	Thr
625					630					635					640
Leu	Leu	Met	Met	Leu	Lys	Asp	Met	His	Asp	Ser	Lys	Thr	Lys	Glu	Gln
				645					650					655	
Arg	Leu	Met	Thr	Ala	Gln	Asn	Leu	Val	Ser	Tyr	Arg	Ser	Pro	Gly	Arg
			660					665					670		
Gly	Asp	Cys	Ser	Thr	Asn	Ser	Pro	Val	Gly	Val	Ser	Lys	Val	Leu	Val
	675						680					685			
Ser	Gly	Gly	Ser	Thr	His	Asn	Ser	Glu	Lys	Lys	Gly	Asp	Gly	Thr	Gln
	690					695					700				
Asn	Ser	Ala	Asn	Pro	Ser	Pro	Ser	Gly	Gly	Asp	Ser	Ala	Leu	Ser	Gly
705					710					715					720
Glu	Leu	Ser	Ala	Ser	Leu	Pro	Gly	Leu	Leu	Ser	Asp	Lys	Arg	Asp	Leu
				725					730					735	
Pro	Ala	Ser	Gly	Lys	Ser	Arg	Ser	Asp	Cys	Val	Thr	Arg	Arg	Asn	Cys
			740					745					750		
Gly	Arg	Ser	Lys	Pro	Ser	Ser	Lys	Leu	Arg	Asp	Ala	Phe	Ser	Ala	Gln
	755						760					765			
Met	Val	Lys	Asn	Thr	Val	Asn	Arg	Lys	Ala	Leu	Lys	Thr	Glu	Arg	Lys
	770					775					780				
Arg	Lys	Leu	Asn	Gln	Leu	Pro	Ser	Val	Thr	Leu	Asp	Ala	Val	Leu	Gln
785					790					795					800
Gly	Asp	Arg	Glu	Arg	Gly	Gly	Ser	Leu	Arg	Gly	Gly	Ala	Glu	Asp	Pro
				805					810					815	
Ser	Lys	Glu	Asp	Pro	Leu	Gln	Ile	Met	Gly	His	Leu	Thr	Ser	Glu	Asp
			820					825					830		
Gly	Asp	His	Phe	Ser	Asp	Val	His	Phe	Asp	Ser	Lys	Val	Lys	Gln	Ser
	835						840					845			
Asp	Pro	Gly	Lys	Ile	Ser	Glu	Lys	Gly	Leu	Ser	Phe	Glu	Asn	Gly	Lys
	850					855					860				
Gly	Pro	Glu	Leu	Asp	Ser	Val	Met	Asn	Ser	Glu	Asn	Asp	Glu	Leu	Asn
865					870					875					880
Gly	Val	Asn	Gln	Val	Val	Pro	Lys	Lys	Arg	Trp	Gln	Arg	Leu	Asn	Gln
				885					890					895	
Arg	Arg	Thr	Lys	Pro	Arg	Lys	Arg	Met	Asn	Arg	Phe	Lys	Glu	Lys	Glu
			900					905					910		
Asn	Ser	Glu	Cys	Ala	Phe	Arg	Val	Leu	Leu	Pro	Ser	Asp	Pro	Val	Gln
			915				920					925			
Glu	Gly	Arg	Asp	Glu	Phe	Pro	Glu	His	Arg	Thr	Pro	Ser	Ala	Ser	Ile
	930					935					940				
Leu	Glu	Glu	Pro	Leu	Thr	Glu	Gln	Asn	His	Ala	Asp	Cys	Leu	Asp	Ser
945					950					955					960
Ala	Gly	Pro	Arg	Leu	Asn	Val	Cys	Asp	Lys	Ser	Ser	Ala	Ser	Ile	Gly
				965					970					975	
Asp	Met	Glu	Lys	Glu	Pro	Gly	Ile	Pro	Ser	Leu	Thr	Pro	Gln	Ala	Glu
			980					985					990		
Leu	Pro	Glu	Pro	Ala	Val	Arg	Ser	Glu	Lys	Lys	Arg	Leu	Arg	Lys	Pro
			995				1000					1005			
Ser	Lys	Trp	Leu	Leu	Glu	Tyr	Thr	Glu	Glu	Tyr	Asp	Gln	Ile	Phe	Ala
			1010				1015					1020			

Pro Lys Lys Lys Gln Lys Lys Val Gln Glu Gln Val His Lys Val Ser																			
1025					1030				1035										1040
Ser Arg Cys Glu Glu Glu Ser Leu Leu Ala Arg Gly Arg Ser Ser Ala					1045				1050										1055
Gln Asn Lys Gln Val Asp Glu Asn Ser Leu Ile Ser Thr Lys Glu Glu					1060				1065										1070
Pro Pro Val Leu Glu Arg Glu Ala Pro Phe Leu Glu Gly Pro Leu Ala					1075				1080										1085
Gln Ser Glu Leu Gly Gly Gly His Ala Glu Leu Pro Gln Leu Thr Leu					1090				1095										1100
Ser Val Pro Val Ala Pro Glu Val Ser Pro Arg Pro Ala Leu Glu Ser					1105				1110										1115
Glu Glu Leu Leu Val Lys Thr Pro Gly Asn Tyr Glu Ser Lys Arg Gln					1120				1125										1130
Arg Lys Pro Thr Lys Lys Leu Leu Glu Ser Asn Asp Leu Asp Pro Gly					1135				1140										1145
Phe Met Pro Lys Lys Gly Asp Leu Gly Leu Ser Lys Lys Cys Tyr Glu					1150				1155										1160
Ala Gly His Leu Glu Asn Gly Ile Thr Glu Ser Cys Ala Thr Ser Tyr					1165				1170										1175
Ser Lys Asp Phe Gly Gly Gly Thr Thr Lys Ile Phe Asp Lys Pro Arg					1180				1185										1190
Lys Arg Lys Arg Gln Arg His Ala Ala Lys Met Gln Cys Lys Lys					1195				1200										1205
Val Lys Asn Asp Asp Ser Ser Lys Glu Ile Pro Gly Ser Glu Gly Glu					1210				1215										1220
Leu Met Pro His Arg Thr Ala Thr Ser Pro Lys Glu Thr Val Glu Glu					1225				1230										1235
Gly Val Glu His Asp Pro Gly Met Pro Ala Ser Lys Lys Met Gln Gly					1240				1245										1250
Glu Arg Gly Gly Gly Ala Ala Leu Lys Glu Asn Val Cys Gln Asn Cys					1255				1260										1265
Glu Lys Leu Gly Glu Leu Leu Leu Cys Glu Ala Gln Cys Cys Gly Ala					1270				1275										1280
Phe His Leu Glu Cys Leu Gly Leu Thr Glu Met Pro Arg Gly Lys Phe					1285				1290										1295
Ile Cys Asn Glu Cys Arg Thr Gly Ile His Thr Cys Phe Val Cys Lys					1300				1305										1310
Gln Ser Gly Glu Asp Val Lys Arg Cys Leu Leu Pro Leu Cys Gly Lys					1315				1320										1325
Phe Tyr His Glu Glu Cys Val Gln Lys Tyr Pro Pro Thr Val Met Gln					1330				1335										1340
Asn Lys Gly Phe Arg Cys Ser Leu His Ile Cys Ile Thr Cys His Ala					1345				1350										1355
Ala Asn Pro Ala Asn Val Ser Ala Ser Lys Gly Arg Leu Met Arg Cys					1365				1370										1375
Val Arg Cys Pro Val Ala Tyr His Ala Asn Asp Phe Cys Leu Ala Ala					1380				1385										1390
Gly Ser Lys Ile Leu Ala Ser Asn Ser Ile Ile Cys Pro Asn His Phe					1395				1400										1405
Thr Pro Arg Arg Gly Cys Arg Asn His Glu His Val Asn Val Ser Trp					1410				1415										1420
Cys Phe Val Cys Ser Glu Gly Gly Ser Leu Leu Cys Cys Asp Ser Cys					1425				1430										1435
Pro Ala Ala Phe His Arg Glu Cys Leu Asn Ile Asp Ile Pro Glu Gly					1440				1445										1450
Asn Trp Tyr Cys Asn Asp Cys Lys Ala Gly Lys Lys Pro His Tyr Arg					1455				1460										1465
Glu Ile Val Trp Val Lys Val Gly Arg Tyr Arg Trp Trp Pro Ala Glu					1470				1475										1480
					1485				1490										1495
																			1500

Ile Cys His Pro Arg Ala Val Pro Ser Asn Ile Asp Lys Met Arg His	1505	1510	1515	1520
Asp Val Gly Glu Phe Pro Val Leu Phe Phe Gly Ser Asn Asp Tyr Leu		1525	1530	1535
Trp Thr His Gln Ala Arg Val Phe Pro Tyr Met Glu Gly Asp Val Ser		1540	1545	1550
Ser Lys Asp Lys Met Gly Lys Gly Val Asp Gly Thr Tyr Lys Lys Ala	1555		1560	1565
Leu Gln Glu Ala Ala Ala Arg Phe Glu Glu Leu Lys Ala Gln Lys Glu	1570	1575	1580	
Leu Arg Gln Leu Gln Glu Asp Arg Lys Asn Asp Lys Lys Pro Pro Pro	1585	1590	1595	1600
Tyr Lys His Ile Lys Val Asn Arg Pro Ile Gly Arg Val Gln Ile Phe		1605	1610	1615
Thr Ala Asp Leu Ser Glu Ile Pro Arg Cys Asn Cys Lys Ala Thr Asp		1620	1625	1630
Glu Asn Pro Cys Gly Ile Asp Ser Glu Cys Ile Asn Arg Met Leu Leu	1635		1640	1645
Tyr Glu Cys His Pro Thr Val Cys Pro Ala Gly Gly Arg Cys Gln Asn	1650	1655	1660	
Gln Cys Phe Ser Lys Arg Gln Tyr Pro Glu Val Glu Ile Phe Arg Thr	1665	1670	1675	1680
Leu Gln Arg Gly Trp Gly Leu Arg Thr Lys Thr Asp Ile Lys Lys Gly		1685	1690	1695
Glu Phe Val Asn Glu Tyr Val Gly Glu Leu Ile Asp Glu Glu Glu Cys		1700	1705	1710
Arg Ala Arg Ile Arg Tyr Ala Gln Glu His Asp Ile Thr Asn Phe Tyr	1715	1720		1725
Met Leu Thr Leu Asp Lys Asp Arg Ile Ile Asp Ala Gly Pro Lys Gly	1730	1735	1740	
Asn Tyr Ala Arg Phe Met Asn His Cys Cys Gln Pro Asn Cys Glu Thr	1745	1750	1755	1760
Gln Lys Trp Ser Val Asn Gly Asp Thr Arg Val Gly Leu Phe Ala Leu		1765	1770	1775
Ser Asp Ile Lys Ala Gly Thr Glu Leu Thr Phe Asn Tyr Asn Leu Glu	1780		1785	1790
Cys Leu Gly Asn Gly Lys Thr Val Cys Lys Cys Gly Ala Pro Asn Cys	1795	1800		1805
Ser Gly Phe Leu Gly Val Arg Pro Lys Asn Gln Pro Ile Ala Thr Glu	1810	1815	1820	
Glu Lys Ser Lys Lys Phe Lys Lys Lys Gln Gln Gly Lys Arg Arg Thr	1825	1830	1835	1840
Gln Gly Glu Ile Thr Lys Glu Arg Glu Asp Glu Cys Phe Ser Cys Gly		1845	1850	1855
Asp Ala Gly Gln Leu Val Ser Cys Lys Lys Pro Gly Cys Pro Lys Val	1860	1865		1870
Tyr His Ala Asp Cys Leu Asn Leu Thr Lys Arg Pro Ala Gly Lys Trp	1875	1880	1885	
Glu Cys Pro Trp His Gln Cys Asp Ile Cys Gly Lys Glu Ala Ala Ser	1890	1895	1900	
Phe Cys Glu Met Cys Pro Ser Ser Phe Cys Lys Gln His Arg Glu Gly	1905	1910	1915	1920
Met Leu Phe Ile Ser Lys Leu Asp Gly Arg Leu Ser Cys Thr Glu His		1925	1930	1935
Asp Pro Cys Gly Pro Asn Pro Leu Glu Pro Gly Glu Ile Arg Glu Tyr	1940	1945		1950
Val Pro Pro Pro Val Pro Leu Pro Pro Gly Pro Ser Thr His Leu Ala	1955	1960	1965	
Glu Gln Ser Thr Gly Met Ala Ala Gln Ala Pro Lys Met Ser Asp Lys	1970	1975	1980	

Pro Pro Ala Asp Thr Asn Gln Met Leu Ser Leu Ser Lys Lys Ala Leu
1985 1990 1995 2000
Ala Gly Thr Cys Gln Arg Pro Leu Leu Pro Glu Arg Pro Leu Glu Arg
2005 2010 2015
Thr Asp Ser Arg Pro Gln Pro Leu Asp Lys Val Arg Asp Leu Ala Gly
2020 2025 2030
Ser Gly Thr Lys Ser Gln Ser Leu Val Ser Ser Gln Arg Pro Leu Asp
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Ser Pro Val Thr Ser Pro Ser Ser Pro Ser Val Arg Ser Gln Pro
2065 2070 2075 2080
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2260 2265 2270
Pro Pro Ala Lys Ala Phe Leu Tyr Glu Pro Thr Thr Gln Ala Ser Gly
2275 2280 2285
Arg Ala Ser Ala Gly Ala Glu Gln Thr Pro Gly Pro Leu Ser Gln Ser
2290 2295 2300
Pro Gly Leu Val Lys Gln Ala Lys Gln Met Val Gly Gly Gln Gln Leu
2305 2310 2315 2320
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2325 2330 2335
Ala Pro Ala Ser Leu Pro Thr Glu Glu Lys Lys Leu Val Thr Thr Glu
2340 2345 2350
Gln Ser Pro Trp Ala Leu Gly Lys Ala Ser Ser Arg Ala Gly Leu Trp
2355 2360 2365
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2370 2375 2380
Ser Thr Gln Thr Leu Ala Gln Thr Cys Trp Ser Leu Gly Arg Gly Gln
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2420 2425

<210> 35

<211> 7707

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence; note =
synthetic construct

<400> 35

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<210> 36

<211> 2696

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence; note =
synthetic construct

<400> 36

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Gly Asn Gly Gln Ser Asn Phe Ser Glu Pro Leu Asn Gly Cys Thr Met
          35          40          45
Gln Leu Ser Thr Val Ser Gly Thr Ser Gln Asn Ala Tyr Gly Gln Asp
 50          55          60
Ser Pro Ser Cys Tyr Ile Pro Leu Arg Arg Leu Gln Asp Leu Ala Ser
65          70          75          80
Met Ile Asn Val Glu Tyr Leu Asn Gly Ser Ala Asp Gly Ser Glu Ser
          85          90          95
Phe Gln Asp Pro Glu Lys Ser Asp Ser Arg Ala Gln Thr Pro Ile Val
          100          105          110
Cys Thr Ser Leu Ser Pro Gly Gly Pro Thr Ala Leu Ala Met Lys Gln
          115          120          125
Glu Pro Ser Cys Asn Asn Ser Pro Glu Leu Gln Val Lys Val Thr Lys
          130          135          140
Thr Ile Lys Asn Gly Phe Leu His Phe Glu Asn Phe Thr Cys Val Asp
          145          150          155          160
Asp Ala Asp Val Asp Ser Glu Met Asp Pro Glu Gln Pro Val Thr Glu
          165          170          175
Asp Glu Ser Ile Glu Glu Ile Phe Glu Glu Thr Gln Thr Asn Ala Thr
          180          185          190
Cys Asn Tyr Glu Thr Lys Ser Glu Asn Gly Val Lys Val Ala Met Gly
          195          200          205
Ser Glu Gln Asp Ser Thr Pro Glu Ser Arg His Gly Ala Val Lys Ser
          210          215          220
Pro Phe Leu Pro Leu Ala Pro Gln Thr Glu Thr Gln Lys Asn Lys Gln
          225          230          235          240
Arg Asn Glu Val Asp Gly Ser Asn Glu Lys Ala Ala Leu Leu Pro Ala
          245          250          255

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Leu	Gly	Asn	Met	Leu	Glu	Leu	Pro	Gly	Thr	Ser	Ser	Ser	Ser	Thr	Ser	290	295	300
Gln	Glu	Leu	Pro	Phe	Cys	Gln	Pro	Lys	Lys	Lys	Ser	Thr	Pro	Leu	Lys	305	310	315
Tyr	Glu	Val	Gly	Asp	Leu	Ile	Trp	Ala	Lys	Phe	Lys	Arg	Arg	Pro	Trp	325	330	335
Trp	Pro	Cys	Arg	Ile	Cys	Ser	Asp	Pro	Leu	Ile	Asn	Thr	His	Ser	Lys	340	345	350
Met	Lys	Val	Ser	Asn	Arg	Arg	Pro	Tyr	Arg	Gln	Tyr	Tyr	Val	Glu	Ala	355	360	365
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Thr	Ala	Lys	Lys	Glu	Phe	Glu	Thr	Ser	Asn	Gly	Asp	Ser	Leu	Leu	Gly	580	585	590
Leu	Pro	Glu	Gly	Ala	Leu	Ile	Ser	Lys	Cys	Ser	Arg	Glu	Lys	Asn	Lys	595	600	605
Pro	Gln	Arg	Ser	Leu	Val	Cys	Gly	Ser	Lys	Val	Lys	Leu	Cys	Tyr	Ile	610	615	620
Gly	Ala	Gly	Asp	Glu	Glu	Lys	Arg	Ser	Asp	Ser	Ile	Ser	Ile	Cys	Thr	625	630	635
Thr	Ser	Asp	Asp	Gly	Ser	Ser	Asp	Leu	Asp	Pro	Ile	Glu	His	Ser	Ser	645	650	655
Glu	Ser	Asp	Asn	Ser	Val	Leu	Glu	Ile	Pro	Asp	Ala	Phe	Asp	Arg	Thr	660	665	670
Glu	Asn	Met	Leu	Ser	Met	Gln	Lys	Asn	Glu	Lys	Ile	Lys	Tyr	Ser	Arg	675	680	685
Phe	Ala	Ala	Thr	Asn	Thr	Arg	Val	Lys	Ala	Lys	Gln	Lys	Pro	Leu	Ile	690	695	700
Ser	Asn	Ser	His	Thr	Asp	His	Leu	Met	Gly	Cys	Thr	Lys	Ser	Ala	Glu	705	710	715
Pro	Gly	Thr	Glu	Thr	Ser	Gln	Val	Asn	Leu	Ser	Asp	Leu	Lys	Ala	Ser	725	730	735

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Lys	Glu	Leu	Ser	Tyr	Arg	Ser	Leu	Gly	Glu	Asp	Val	Ser	Asp	Ser	Gly		
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Thr	Ser	Lys	Pro	Ser	Lys	Pro	Leu	Leu	Phe	Ser	Ser	Ala	Ser	Ser	Gln		
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Asn	His	Ile	Pro	Ile	Glu	Pro	Asp	Tyr	Lys	Phe	Ser	Thr	Leu	Leu	Met		
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Thr	Ala	Gln	Asn	Leu	Val	Ser	Tyr	Arg	Ser	Pro	Gly	Arg	Gly	Asp	Cys		
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Ser	Thr	Asn	Ser	Pro	Val	Gly	Val	Ser	Lys	Val	Leu	Val	Ser	Gly	Gly		
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Pro	Ala	Val	Arg	Ser	Glu	Lys	Lys	Arg	Leu	Arg	Lys	Pro	Ser	Lys	Trp	1265	1270	1275
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Lys	Gln	Lys	Lys	Val	Gln	Glu	Gln	Val	His	Lys	Val	Ser	Ser	Arg	Cys	1300	1305	1310
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Gln	Val	Asp	Glu	Asn	Ser	Leu	Ile	Ser	Thr	Lys	Glu	Glu	Pro	Pro	Val	1330	1335	1340
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Lys	Lys	Gly	Asp	Leu	Gly	Leu	Ser	Lys	Lys	Cys	Tyr	Glu	Ala	Gly	His	1425	1430	1435
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Phe	Gly	Gly	Gly	Thr	Thr	Lys	Ile	Phe	Asp	Lys	Pro	Arg	Lys	Arg	Lys	1460	1465	1470
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Glu	Glu	Cys	Val	Gln	Lys	Tyr	Pro	Pro	Thr	Val	Met	Gln	Asn	Lys	Gly	1620	1625	1630
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Pro	Val	Ala	Tyr	His	Ala	Asn	Asp	Phe	Cys	Leu	Ala	Ala	Gly	Ser	Lys	1665	1670	1675
Ile	Leu	Ala	Ser	Asn	Ser	Ile	Ile	Cys	Pro	Asn	His	Phe	Thr	Pro	Arg	1685	1690	1695

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Pro	Arg	Ala	Val	Pro	Ser	Asn	Ile	Asp	Lys	Met	Arg	His	Asp	Val	Gly
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Ala	Ala	Ala	Arg	Phe	Glu	Glu	Leu	Lys	Ala	Gln	Lys	Glu	Leu	Arg	Gln
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 Lys Cys Ala Glu Ser Glu Gln Lys
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<210> 38

<211> 1784

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence; note =
synthetic construct

<400> 38

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Arg Leu Leu Glu Glu Asp Thr Pro Arg Tyr Met Arg Ala Ser Asp Pro
      35             40             45
Ala Ser Pro His Ile Gly Arg Ser Asn Glu Glu Glu Glu Thr Ser Asp
      50             55             60
Ser Ser Leu Glu Lys Gln Thr Arg Ser Lys Tyr Cys Thr Glu Thr Ser
65             70             75             80

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Ser	Leu	Glu	Ser	Lys	Ala	Glu	Arg	Ile	Ala	Arg	Tyr	Lys	Ala	Glu	Arg	
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Arg	Arg	Gln	Leu	Ala	Glu	Lys	Tyr	Gly	Leu	Thr	Leu	Asp	Pro	Glu	Ala	
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Asp	Ser	Glu	Tyr	Leu	Ser	Arg	Tyr	Thr	Lys	Ser	Arg	Lys	Glu	Pro	Asp	
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Thr	Cys	Ala	Gly	Glu	Ser	Lys	Asp	Tyr	Ala	Leu	His	Ala	Gly	Asp	Gly	
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Gln	Glu	Leu	Ser	Ala	Thr	Arg	Gln	Ala	His	Asp	Leu	Ser	Pro	Ala	Ala	
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Glu	Ser	Ser	Ser	Thr	Phe	Ser	Phe	Ser	Gly	Arg	Asp	Ser	Ser	Phe	Thr	
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Glu	Val	Pro	Arg	Ser	Pro	Lys	His	Ala	His	Ser	Ser	Ser	Leu	Gln	Gln	
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Ala	Ala	Ser	Arg	Ser	Pro	Ser	Phe	Gly	Asp	Pro	Gln	Leu	Ser	Pro	Glu	
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Ala	Arg	Pro	Arg	Cys	Thr	Ser	His	Ser	Glu	Thr	Pro	Thr	Val	Asp	Asp	
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Glu	Glu	Lys	Val	Asp	Glu	Arg	Ala	Lys	Leu	Ser	Val	Ala	Ala	Lys	Arg	
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Leu	Leu	Phe	Arg	Glu	Met	Glu	Lys	Ser	Phe	Asp	Glu	Gln	Asn	Val	Pro	
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Lys	Arg	Arg	Ser	Arg	Asn	Thr	Ala	Val	Glu	Gln	Arg	Leu	Arg	Arg	Leu	
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Gln	Asp	Arg	Ser	Leu	Thr	Gln	Pro	Ile	Thr	Thr	Glu	Glu	Val	Val	Ile	
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Gln	Arg	Arg	Met	Asn	Ala	Arg	Tyr	Gln	Thr	Gln	Pro	Val	Thr	Leu	Gly	
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Glu	Val	Glu	Gln	Val	Gln	Ser	Gly	Lys	Leu	Ile	Pro	Phe	Ser	Pro	Ala	
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Val	Asn	Thr	Ser	Val	Ser	Thr	Val	Ala	Ser	Thr	Val	Ala	Pro	Met	Tyr	
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Ala	Gly	Asp	Leu	Arg	Thr	Lys	Pro	Pro	Leu	Asp	His	Asn	Ala	Ser	Ala	
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Glu	Asn	Lys	Gly	Met	Leu	Arg	Glu	Tyr	Gly	Glu	Thr	Glu	Ser	Lys	Arg	
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Glu	Ala	Glu	Ala	Ser	Tyr	Pro	Ile	Leu	Asn	Arg	Ala	Arg	Glu	Gly	Asp	
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 580 585 590
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 Ser Arg Arg Gln Glu Gly Gly Lys Ala Pro Ala Ser Ser Leu His Thr
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 Gln Glu Ala Gly Arg Ser Leu Ile Lys Lys Arg Val Thr Glu Ser Arg
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Gln Pro Ala Leu Phe Leu Val Asp Asn His His Glu Val Tyr Leu Trp
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Gln Gly Trp Trp Pro Ile Glu Asn Lys Ile Thr Gly Ser Ala Arg Ile
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Arg Trp Ala Ser Asp Arg Lys Ser Ala Met Glu Thr Val Leu Gln Tyr
1650 1655 1660
Cys Lys Gly Lys Asn Leu Lys Lys Pro Ala Pro Lys Ser Tyr Leu Ile
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His Ala Gly Leu Glu Pro Leu Thr Phe Thr Asn Met Phe Pro Ser Trp
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Glu His Arg Glu Asp Ile Ala Glu Ile Thr Glu Met Asp Thr Glu Val
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Ser Asn Gln Ile Thr Leu Val Glu Asp Val Leu Ala Lys Leu Cys Lys
1715 1720 1725
Thr Ile Tyr Pro Leu Ala Asp Leu Leu Ala Arg Pro Leu Pro Glu Gly
1730 1735 1740
Val Asp Pro Leu Lys Leu Glu Ile Tyr Leu Thr Asp Glu Asp Phe Glu
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1780

<210> 39

<211> 6719

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence; note =
synthetic construct

<400> 39

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<210> 40

<211> 731

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence; note =
synthetic construct

<400> 40

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Leu	Gln	Ile	Trp	Arg	Val	Glu	Lys	Phe	Asp	Leu	Val	Pro	Val	Pro	Pro
			20					25					30		
Asn	Leu	Tyr	Gly	Asp	Phe	Phe	Thr	Gly	Asp	Ala	Tyr	Val	Ile	Leu	Lys
		35					40					45			
Thr	Val	Gln	Leu	Arg	Asn	Gly	Asn	Leu	Gln	Tyr	Asp	Leu	His	Tyr	Trp
	50					55					60				
Leu	Gly	Asn	Glu	Cys	Ser	Gln	Asp	Glu	Ser	Gly	Ala	Ala	Ala	Ile	Phe
65					70					75				80	
Thr	Val	Gln	Leu	Asp	Asp	Tyr	Leu	Asn	Gly	Arg	Ala	Val	Gln	His	Arg
			85					90						95	

Glu	Val	Gln	Gly	Phe	Glu	Ser	Ser	Thr	Phe	Ser	Gly	Tyr	Phe	Lys	Ser	100	105	110
Gly	Leu	Lys	Tyr	Lys	Lys	Gly	Gly	Val	Ala	Ser	Gly	Phe	Lys	His	Val	115	120	125
Val	Pro	Asn	Glu	Val	Val	Val	Gln	Arg	Leu	Phe	Gln	Val	Lys	Gly	Arg	130	135	140
Arg	Val	Val	Arg	Ala	Thr	Glu	Val	Pro	Val	Ser	Trp	Asp	Ser	Phe	Asn	145	150	155
Asn	Gly	Asp	Cys	Phe	Ile	Leu	Asp	Leu	Gly	Asn	Asn	Ile	Tyr	Gln	Trp	165	170	175
Cys	Gly	Ser	Gly	Ser	Asn	Lys	Phe	Glu	Arg	Leu	Lys	Ala	Thr	Gln	Val	180	185	190
Ser	Lys	Gly	Ile	Arg	Asp	Asn	Glu	Arg	Ser	Gly	Arg	Ala	Gln	Val	His	195	200	205
Val	Ser	Glu	Glu	Glu	Thr	Glu	Pro	Glu	Ala	Met	Leu	Gln	Val	Leu	Gly	210	215	220
Pro	Lys	Pro	Ala	Leu	Pro	Glu	Gly	Thr	Glu	Asp	Thr	Ala	Lys	Glu	Asp	225	230	235
Ala	Ala	Asn	Arg	Lys	Leu	Ala	Lys	Leu	Tyr	Lys	Val	Ser	Asn	Gly	Ala	245	250	255
Gly	Ser	Met	Ser	Val	Ser	Leu	Val	Ala	Asp	Glu	Asn	Pro	Phe	Ala	Gln	260	265	270
Gly	Pro	Leu	Arg	Ser	Glu	Asp	Cys	Phe	Ile	Leu	Asp	His	Gly	Arg	Asp	275	280	285
Gly	Lys	Ile	Phe	Val	Trp	Lys	Gly	Lys	Gln	Ala	Asn	Met	Glu	Glu	Arg	290	295	300
Lys	Ala	Ala	Leu	Lys	Thr	Ala	Ser	Asp	Phe	Ile	Ser	Lys	Met	Gln	Tyr	305	310	315
Pro	Arg	Gln	Thr	Gln	Val	Ser	Val	Leu	Pro	Glu	Gly	Gly	Glu	Thr	Pro	325	330	335
Leu	Phe	Lys	Gln	Phe	Phe	Lys	Asn	Trp	Arg	Asp	Pro	Asp	Gln	Thr	Asp	340	345	350
Gly	Pro	Gly	Leu	Gly	Tyr	Leu	Ser	Ser	His	Ile	Ala	Asn	Val	Glu	Arg	355	360	365
Val	Pro	Phe	Asp	Ala	Gly	Thr	Leu	His	Thr	Ser	Thr	Ala	Met	Ala	Ala	370	375	380
Gln	His	Gly	Met	Asp	Asp	Asp	Gly	Thr	Gly	Gln	Lys	Gln	Ile	Trp	Arg	385	390	395
Ile	Glu	Gly	Ser	Asn	Lys	Val	Pro	Val	Asp	Pro	Ala	Thr	Tyr	Gly	Gln	405	410	415
Phe	Tyr	Gly	Gly	Asp	Ser	Tyr	Ile	Ile	Leu	Tyr	Asn	Tyr	Arg	His	Gly	420	425	430
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Gln	Asp	Glu	Val	Ala	Ala	Ser	Ala	Ile	Leu	Thr	Ala	Gln	Leu	Asp	Glu	450	455	460
Glu	Leu	Gly	Gly	Thr	Pro	Val	Gln	Ser	Arg	Val	Val	Gln	Gly	Lys	Glu	465	470	475
Pro	Ala	His	Leu	Met	Ser	Leu	Phe	Gly	Gly	Lys	Pro	Met	Ile	Ile	Tyr	485	490	495
Lys	Gly	Gly	Thr	Ser	Arg	Asp	Gly	Gly	Gln	Thr	Ala	Pro	Ala	Ser	Ile	500	505	510
Arg	Leu	Phe	Gln	Val	Arg	Ala	Ser	Ser	Ser	Gly	Ala	Thr	Arg	Ala	Val	515	520	525
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Leu	Lys	Thr	Pro	Ser	Ala	Ala	Tyr	Leu	Trp	Val	Gly	Ala	Gly	Ala	Ser	545	550	555
Glu	Ala	Glu	Lys	Thr	Ala	Ala	Gln	Glu	Leu	Leu	Lys	Val	Leu	Arg	Ser	565	570	575


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<210> 42

<211> 928

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence; note =
synthetic construct

<400> 42

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Pro Glu Gln Asp Ser Gly Pro Glu Asp Leu Pro Leu Val Arg Leu Glu
          35          40          45
Phe Glu Glu Thr Glu Glu Pro Asp Phe Thr Ala Leu Cys Gln Lys Leu
          50          55          60
Lys Ile Pro Asp His Val Arg Glu Arg Ala Trp Leu Thr Trp Glu Lys
          65          70          75          80
Val Ser Ser Val Asp Gly Val Leu Gly Gly Tyr Ile Gln Lys Lys Lys
          85          90          95
Glu Leu Trp Gly Ile Cys Ile Phe Ile Ala Ala Val Asp Leu Asp Glu
          100          105          110
Met Ser Phe Thr Phe Thr Glu Leu Gln Lys Asn Ile Glu Ile Ser Val
          115          120          125
His Lys Phe Phe Asn Leu Leu Lys Glu Ile Asp Thr Ser Thr Lys Val
          130          135          140
Asp Asn Ala Met Ser Arg Leu Leu Lys Lys Tyr Asp Val Leu Phe Ala
          145          150          155          160
Leu Phe Ser Lys Leu Glu Arg Thr Cys Glu Leu Ile Tyr Leu Thr Gln
          165          170          175
Pro Ser Ser Ser Ile Ser Thr Glu Ile Asn Ser Ala Leu Val Leu Lys
          180          185          190
Val Ser Trp Ile Thr Phe Leu Leu Ala Lys Gly Glu Val Leu Gln Met
          195          200          205
Glu Asp Asp Leu Val Ile Ser Phe Gln Leu Met Leu Cys Val Leu Asp
          210          215          220
Tyr Phe Ile Lys Leu Ser Pro Pro Met Leu Leu Lys Glu Pro Tyr Lys
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Thr Ala Val Ile Pro Ile Asn Gly Ser Pro Arg Thr Pro Arg Arg Gly
          245          250          255
Gln Asn Arg Ser Ala Arg Ile Ala Lys Gln Leu Glu Asn Asp Thr Arg
          260          265          270
Ile Ile Glu Val Leu Cys Lys Glu His Glu Cys Asn Ile Asp Glu Val
          275          280          285
Lys Asn Val Tyr Phe Lys Asn Phe Ile Pro Phe Met Asn Ser Leu Gly
          290          295          300

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Leu	Asp	His	Asp	Lys	Thr	Leu	Gln	Thr	Asp	Ser	Ile	Asp	Ser	Phe	Glu	340	345	350	
Thr	Gln	Arg	Thr	Pro	Arg	Lys	Ser	Asn	Leu	Asp	Glu	Glu	Val	Asn	Val	355	360	365	
Ile	Pro	Pro	His	Thr	Pro	Val	Arg	Thr	Val	Met	Asn	Thr	Ile	Gln	Gln	370	375	380	
Leu	Met	Met	Ile	Leu	Asn	Ser	Ala	Ser	Asp	Gln	Pro	Ser	Glu	Asn	Leu	385	390	395	400
Ile	Ser	Tyr	Phe	Asn	Asn	Cys	Thr	Val	Asn	Pro	Lys	Glu	Ser	Ile	Leu	405	410	415	
Lys	Arg	Val	Lys	Asp	Ile	Gly	Tyr	Ile	Phe	Lys	Glu	Lys	Phe	Ala	Lys	420	425	430	
Ala	Val	Gly	Gln	Gly	Cys	Val	Glu	Ile	Gly	Ser	Gln	Arg	Tyr	Lys	Leu	435	440	445	
Gly	Val	Arg	Leu	Tyr	Tyr	Arg	Val	Met	Glu	Ser	Met	Leu	Lys	Ser	Glu	450	455	460	
Glu	Glu	Arg	Leu	Ser	Ile	Gln	Asn	Phe	Ser	Lys	Leu	Leu	Asn	Asp	Asn	465	470	475	480
Ile	Phe	His	Met	Ser	Leu	Leu	Ala	Cys	Ala	Leu	Glu	Val	Val	Met	Ala	485	490	495	
Thr	Tyr	Ser	Arg	Ser	Thr	Ser	Gln	Asn	Leu	Asp	Ser	Gly	Thr	Asp	Leu	500	505	510	
Ser	Phe	Pro	Trp	Ile	Leu	Asn	Val	Leu	Asn	Leu	Lys	Ala	Phe	Asp	Phe	515	520	525	
Tyr	Lys	Val	Ile	Glu	Ser	Phe	Ile	Lys	Ala	Glu	Gly	Asn	Leu	Thr	Arg	530	535	540	
Glu	Met	Ile	Lys	His	Leu	Glu	Arg	Cys	Glu	His	Arg	Ile	Met	Glu	Ser	545	550	555	560
Leu	Ala	Trp	Leu	Ser	Asp	Ser	Pro	Leu	Phe	Asp	Leu	Ile	Lys	Gln	Ser	565	570	575	
Lys	Asp	Arg	Glu	Gly	Pro	Thr	Asp	His	Leu	Glu	Ser	Ala	Cys	Pro	Leu	580	585	590	
Asn	Leu	Pro	Leu	Gln	Asn	Asn	His	Thr	Ala	Ala	Asp	Met	Tyr	Leu	Ser	595	600	605	
Pro	Val	Arg	Ser	Pro	Lys	Lys	Lys	Gly	Ser	Thr	Thr	Arg	Val	Asn	Ser	610	615	620	
Thr	Ala	Asn	Ala	Glu	Thr	Gln	Ala	Thr	Ser	Ala	Phe	Gln	Thr	Gln	Lys	625	630	635	640
Pro	Leu	Lys	Ser	Thr	Ser	Leu	Ser	Leu	Phe	Tyr	Lys	Lys	Val	Tyr	Arg	645	650	655	
Leu	Ala	Tyr	Leu	Arg	Leu	Asn	Thr	Leu	Cys	Glu	Arg	Leu	Leu	Ser	Glu	660	665	670	
His	Pro	Glu	Leu	Glu	His	Ile	Ile	Trp	Thr	Leu	Phe	Gln	His	Thr	Leu	675	680	685	
Gln	Asn	Glu	Tyr	Glu	Leu	Met	Arg	Asp	Arg	His	Leu	Asp	Gln	Ile	Met	690	695	700	
Met	Cys	Ser	Met	Tyr	Gly	Ile	Cys	Lys	Val	Lys	Asn	Ile	Asp	Leu	Lys	705	710	715	720
Phe	Lys	Ile	Ile	Val	Thr	Ala	Tyr	Lys	Asp	Leu	Pro	His	Ala	Val	Gln	725	730	735	
Glu	Thr	Phe	Lys	Arg	Val	Leu	Ile	Lys	Glu	Glu	Glu	Tyr	Asp	Ser	Ile	740	745	750	
Ile	Val	Phe	Tyr	Asn	Ser	Val	Phe	Met	Gln	Arg	Leu	Lys	Thr	Asn	Ile	755	760	765	
Leu	Gln	Tyr	Ala	Ser	Thr	Arg	Pro	Pro	Thr	Leu	Ser	Pro	Ile	Pro	His	770	775	780	

Ile	Pro	Arg	Ser	Pro	Tyr	Lys	Phe	Pro	Ser	Ser	Pro	Leu	Arg	Ile	Pro
785					790					795					800
Gly	Gly	Asn	Ile	Tyr	Ile	Ser	Pro	Leu	Lys	Ser	Pro	Tyr	Lys	Ile	Ser
			805						810					815	
Glu	Gly	Leu	Pro	Thr	Pro	Thr	Lys	Met	Thr	Pro	Arg	Ser	Arg	Ile	Leu
			820					825					830		
Val	Ser	Ile	Gly	Glu	Ser	Phe	Gly	Thr	Ser	Glu	Lys	Phe	Gln	Lys	Ile
		835				840						845			
Asn	Gln	Met	Val	Cys	Asn	Ser	Asp	Arg	Val	Leu	Lys	Arg	Ser	Ala	Glu
	850					855					860				
Gly	Ser	Asn	Pro	Pro	Lys	Pro	Leu	Lys	Lys	Leu	Arg	Phe	Asp	Ile	Glu
865					870					875					880
Gly	Ser	Asp	Glu	Ala	Asp	Gly	Ser	Lys	His	Leu	Pro	Gly	Glu	Ser	Lys
			885					890						895	
Phe	Gln	Gln	Lys	Leu	Ala	Glu	Met	Thr	Ser	Thr	Arg	Thr	Arg	Met	Gln
			900					905					910		
Lys	Gln	Lys	Met	Asn	Asp	Ser	Met	Asp	Thr	Ser	Asn	Lys	Glu	Glu	Lys
	915						920						925		

<210> 43

<211> 2994

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence; note =
synthetic construct

<400> 43

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ggcgtgcccc	gcgtgcgcgc	gcgtcgctct	ccccggcgct	cctccacagc	tcgctggctc	120
ccgccgcgga	aaggcgatcat	gccgccc aaa	accccccgaa	aaacggccgc	caccgccgcc	180
gctgccgccc	cggaaccccc	ggcaccgccc	ccgccgcccc	ctcctgagga	ggacccagag	240
caggacagcg	gcccggagga	cctgcctctc	gtcaggcttg	agtttgaaga	aacagaagaa	300
cctgatTTta	ctgcattatg	tcagaaatta	aagataccag	atcatgtcag	agagagagct	360
tggTTaaact	gggagaaaagt	ttcatctgtg	gatggagtat	tgggaggtta	tattcaaaag	420
aaaaaggaac	tgtggggaaat	ctgtatcttt	attgcagcag	ttgacctaga	tgagatgtcg	480
ttcactTTta	ctgagctaca	gaaaaacata	gaaatcagtg	tccataaaatt	ctttaactta	540
ctaaaagaaa	ttgataccag	taccaaagtt	gataatgcta	tgtcaagact	gttgaagaag	600
tatgatgtat	tgtttgcact	cttcagcaaa	ttggaaagga	catgtgaact	tatatatttg	660
acacaaccca	gcagttcgat	atctactgaa	ataaattctg	cattggtgct	aaaagtttct	720
tggatcacat	ttttattagc	taaaggggaa	gtattacaaa	tggaaagatga	tctggtgatt	780
tcatttcagt	taatgctatg	tgtccttgac	tattttatta	aactctcacc	tcccatggtg	840
ctcaaagaac	catataaaaac	agctgttata	cccattaatg	gttcacctcg	aacaccagg	900
cgaggtcaga	acaggagtgc	acggatagca	aaacaactag	aaaatgatac	aagaattatt	960
gaagttctct	gtaaagaaca	tgaatgtaat	atagatgagg	tgaaaaatgt	ttatttcaaa	1020
aattttatac	cttttatgaa	ttctcttgga	cttgtaacat	ctaattggact	tccagagggt	1080
gaaaatcttt	ctaaacgata	cgaagaaatt	tatcttataa	ataaagatct	agatgcaaga	1140
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agaacaccac	gaaaaagtaa	ccttgatgaa	gaggtgaatg	taattcctcc	acacactcca	1260
gttaggactg	ttatgaacac	tatccaacaa	ttaatgatga	ttttaaatc	agcaagtgat	1320
caaccttcag	aaaatctgat	ttcctatTTt	aacaactgca	cagtgaatcc	aaaagaaagt	1380
atactgaaaa	gagtgaagga	tataggatac	atcttttaaag	agaaatttgc	taaagctgtg	1440
ggacagggtt	gtgtcgaaat	tggatcacag	cgatacaaac	ttggagttcg	cttgatttac	1500
cgagtaatgg	aatccatgct	taaatcagaa	gaagaacgat	tatccattca	aaatttttagc	1560
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atggccacat	atagcagaag	tacatctcag	aatcttgatt	ctggaacaga	tttgtctttc	1680
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tttatcaaa	cagaaggcaa	cttgacaaga	gaaatgataa	aacattttaga	acgatgtgaa	1800
catcgaatca	tggaaatccct	tgcattggctc	tcagattcac	ctttatttga	tcttattaaa	1860
caatcaaagg	accgagaagg	accaactgat	caccttgaat	ctgcttgctc	tcttaattctt	1920

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cctctccaga ataatcacac tgcagcagat atgtatcttt ctctgtgaag atctccaaag 1980
aaaaaagggt caactacgcy tgtaaattct actgcaaata cagagacaca agcaacctca 2040
gccttccaga ccagaaagcc attgaaatct acctctcttt cactgtttta taaaaaagtg 2100
tateggctag cctatctccg gctaaatata ctttgtgaac gccttctgtc tgagcaccca 2160
gaattagaac atatcatctg gacccttttc cagcacaccc tgcagaatga gtatgaactc 2220
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gttcaggaga cattcaaacg tgttttgatc aaagaagagg agtatgattc tattatagta 2400
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aggcccccta ccttgtcacc aatacctcac attcctcgaa gcccttacia gtttcctagt 2520
tcacccttac ggattcctgg agggaacatc tatatttcac ccctgaagag tccatataaa 2580
atttcagaag gtctgccaac accaacaata atgactccaa gatcaagaat cttagtatca 2640
attgggtgaat cattcgggac ttctgagaag ttccagaaaa taaatcagat ggtatgtaac 2700
agcgaccgtg tgctcaaaaag aagtgttgaa ggaagcaacc ctcctaaacc actgaaaaaa 2760
ctacgctttg atattgaagg atcagatgaa gcagatggaa gtaaaccatct cccaggagag 2820
tccaaatttc agcagaaact ggcagaaatg acttctactc gaacacgaat gcaaaagcag 2880
aaaatgaatg atagcatgga tacctcaaac aaggaagaga aatgaggatc tcaggacctt 2940
ggtggacact gtgtacacct ctggattcat tgtctctcac agatgtgact gtat 2994

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<210> 44

<211> 782

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence; note =
synthetic construct

<400> 44

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Met Ala Pro His Arg Pro Ala Pro Ala Leu Leu Cys Ala Leu Ser Leu
 1           5           10          15
Ala Leu Cys Ala Leu Ser Leu Pro Val Arg Ala Ala Thr Ala Ser Arg
 20          25          30
Gly Ala Ser Gln Ala Gly Ala Pro Gln Gly Arg Val Pro Glu Ala Arg
 35          40          45
Pro Asn Ser Met Val Val Glu His Pro Glu Phe Leu Lys Ala Gly Lys
 50          55          60
Glu Pro Gly Leu Gln Ile Trp Arg Val Glu Lys Phe Asp Leu Val Pro
 65          70          75          80
Val Pro Thr Asn Leu Tyr Gly Asp Phe Phe Thr Gly Asp Ala Tyr Val
 85          90          95
Ile Leu Lys Thr Val Gln Leu Arg Asn Gly Asn Leu Gln Tyr Asp Leu
100         105         110
His Tyr Trp Leu Gly Asn Glu Cys Ser Gln Asp Glu Ser Gly Ala Ala
115         120         125
Ala Ile Phe Thr Val Gln Leu Asp Asp Tyr Leu Asn Gly Arg Ala Val
130         135         140
Gln His Arg Glu Val Gln Gly Phe Glu Ser Ala Thr Phe Leu Gly Tyr
145         150         155         160
Phe Lys Ser Gly Leu Lys Tyr Lys Lys Gly Gly Val Ala Ser Gly Phe
165         170         175
Lys His Val Val Pro Asn Glu Val Val Val Gln Arg Leu Phe Gln Val
180         185         190
Lys Gly Arg Arg Val Val Arg Ala Thr Glu Val Pro Val Ser Trp Glu
195         200         205
Ser Phe Asn Asn Gly Asp Cys Phe Ile Leu Asp Leu Gly Asn Asn Ile
210         215         220
His Gln Trp Cys Gly Ser Asn Ser Asn Arg Tyr Glu Arg Leu Lys Ala
225         230         235         240

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Thr	Gln	Val	Ser	Lys	Gly	Ile	Arg	Asp	Asn	Glu	Arg	Ser	Gly	Arg	Ala		
				245					250					255			
Arg	Val	His	Val	Ser	Glu	Glu	Gly	Thr	Glu	Pro	Glu	Ala	Met	Leu	Gln		
			260					265					270				
Val	Leu	Gly	Pro	Lys	Pro	Ala	Leu	Pro	Ala	Gly	Thr	Glu	Asp	Thr	Ala		
		275					280					285					
Lys	Glu	Asp	Ala	Ala	Asn	Arg	Lys	Leu	Ala	Lys	Leu	Tyr	Lys	Val	Ser		
	290				295						300						
Asn	Gly	Ala	Gly	Thr	Met	Ser	Val	Ser	Leu	Val	Ala	Asp	Glu	Asn	Pro		
305					310					315					320		
Phe	Ala	Gln	Gly	Ala	Leu	Lys	Ser	Glu	Asp	Cys	Phe	Ile	Leu	Asp	His		
				325					330					335			
Gly	Lys	Asp	Gly	Lys	Ile	Phe	Val	Trp	Lys	Gly	Lys	Gln	Ala	Asn	Thr		
			340					345					350				
Glu	Glu	Arg	Lys	Ala	Ala	Leu	Lys	Thr	Ala	Ser	Asp	Phe	Ile	Thr	Lys		
			355					360				365					
Met	Asp	Tyr	Pro	Lys	Gln	Thr	Gln	Val	Ser	Val	Leu	Pro	Glu	Gly	Gly		
	370					375					380						
Glu	Thr	Pro	Leu	Phe	Lys	Gln	Phe	Phe	Lys	Asn	Trp	Arg	Asp	Pro	Asp		
385					390					395					400		
Gln	Thr	Asp	Gly	Leu	Gly	Leu	Ser	Tyr	Leu	Ser	Ser	His	Ile	Ala	Asn		
				405					410					415			
Val	Glu	Arg	Val	Pro	Phe	Asp	Ala	Ala	Thr	Leu	His	Thr	Ser	Thr	Ala		
			420					425					430				
Met	Ala	Ala	Gln	His	Gly	Met	Asp	Asp	Asp	Gly	Thr	Gly	Gln	Lys	Gln		
	435					440						445					
Ile	Trp	Arg	Ile	Glu	Gly	Ser	Asn	Lys	Val	Pro	Val	Asp	Pro	Ala	Thr		
	450					455					460						
Tyr	Gly	Gln	Phe	Tyr	Gly	Gly	Asp	Ser	Tyr	Ile	Ile	Leu	Tyr	Asn	Tyr		
465					470					475					480		
Arg	His	Gly	Gly	Arg	Gln	Gly	Gln	Ile	Ile	Tyr	Asn	Trp	Gln	Gly	Ala		
				485					490					495			
Gln	Ser	Thr	Gln	Asp	Glu	Val	Ala	Ala	Ser	Ala	Ile	Leu	Thr	Ala	Gln		
			500					505					510				
Leu	Asp	Glu	Glu	Leu	Gly	Gly	Thr	Pro	Val	Gln	Ser	Arg	Val	Val	Gln		
	515						520					525					
Gly	Lys	Glu	Pro	Ala	His	Leu	Met	Ser	Leu	Phe	Gly	Gly	Lys	Pro	Met		
	530					535					540						
Ile	Ile	Tyr	Lys	Gly	Gly	Thr	Ser	Arg	Glu	Gly	Gly	Gln	Thr	Ala	Pro		
545					550					555					560		
Ala	Ser	Thr	Arg	Leu	Phe	Gln	Val	Arg	Ala	Asn	Ser	Ala	Gly	Ala	Thr		
				565					570					575			
Arg	Ala	Val	Glu	Val	Leu	Pro	Lys	Ala	Gly	Ala	Leu	Asn	Ser	Asn	Asp		
			580					585					590				
Ala	Phe	Val	Leu	Lys	Thr	Pro	Ser	Ala	Ala	Tyr	Leu	Trp	Val	Gly	Thr		
	595						600					605					
Gly	Ala	Ser	Glu	Ala	Glu	Lys	Thr	Gly	Ala	Gln	Glu	Leu	Leu	Arg	Val		
	610					615					620						
Leu	Arg	Ala	Gln	Pro	Val	Gln	Val	Ala	Glu	Gly	Ser	Glu	Pro	Asp	Gly		
625					630					635					640		
Phe	Trp	Glu	Ala	Leu	Gly	Gly	Lys	Ala	Ala	Tyr	Arg	Thr	Ser	Pro	Arg		
				645					650					655			
Leu	Lys	Asp	Lys	Lys	Met	Asp	Ala	His	Pro	Pro	Arg	Leu	Phe	Ala	Cys		
			660					665					670				
Ser	Asn	Lys	Ile	Gly	Arg	Phe	Val	Ile	Glu	Glu	Val	Pro	Gly	Glu	Leu		
	675						680					685					
Met	Gln	Glu	Asp	Leu	Ala	Thr	Asp	Asp	Val	Met	Leu	Leu	Asp	Thr	Trp		
	690					695					700						
Asp	Gln	Val	Phe	Val	Trp	Val	Gly	Lys	Asp	Ser	Gln	Glu	Glu	Glu	Lys		
705					710					715					720		

Thr	Glu	Ala	Leu	Thr	Ser	Ala	Lys	Arg	Tyr	Ile	Glu	Thr	Asp	Pro	Ala
				725					730					735	
Asn	Arg	Asp	Arg	Arg	Thr	Pro	Ile	Thr	Val	Val	Lys	Gln	Gly	Phe	Glu
			740					745					750		
Pro	Pro	Ser	Phe	Val	Gly	Trp	Phe	Leu	Gly	Trp	Asp	Asp	Asp	Tyr	Trp
		755					760				765				
Ser	Val	Asp	Pro	Leu	Asp	Arg	Ala	Met	Ala	Glu	Leu	Ala	Ala		
	770					775					780				

<210> 45

<211> 2663

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence; note =
synthetic construct

<400> 45

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cgccccaggg	gcgggtgccc	gaggcgccgc	ccaacagcat	ggtggtggaa	caccccgagt	180
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tgcccgtgcc	caccaacctt	tatggagact	tcttcacggg	cgacgcctac	gtcatcctga	300
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agtgcagcca	ggatgagagc	ggggcgcccg	ccatctttac	cgtgcagctg	gatgactacc	420
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gctacttcaa	gtctggcctg	aagtacaaga	aaggaggtgt	ggcatcagga	ttcaagcacg	540
tggtagccaa	cgagggtgtg	gtgcagagac	tcttcagggt	caaagggcgg	cgtgtgggtcc	600
gtgccaccga	gggacctgtg	tcctgggaga	gcttcaacaa	tggcgactgc	ttcatcctgg	660
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cagagtcctt gcaaaattgt ctaaaatgtc agtgtttggg aaattaaatc caataaaaaac 2580

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 aaaaaaaaaa aaaaaaaaaa aaa 2663

<210> 46
 <211> 1441
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence; note =
 synthetic construct

<400> 46
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 His Lys Arg Lys Gly Ser Pro Cys Asp Thr Leu Ala Ser Ser Thr Glu
 20 25 30
 Lys Arg Arg Arg Glu Gln Glu Asn Lys Tyr Leu Glu Glu Leu Ala Glu
 35 40 45
 Leu Leu Ser Ala Asn Ile Ser Asp Ile Asp Ser Leu Ser Val Lys Pro
 50 55 60
 Asp Lys Cys Lys Ile Leu Lys Lys Thr Val Asp Gln Ile Gln Leu Met
 65 70 75 80
 Lys Arg Met Glu Gln Glu Lys Ser Thr Thr Asp Asp Asp Val Gln Lys
 85 90 95
 Ser Asp Ile Ser Ser Ser Ser Gln Gly Val Ile Glu Lys Glu Ser Leu
 100 105 110
 Gly Pro Leu Leu Leu Glu Ala Leu Asp Gly Phe Phe Phe Val Val Asn
 115 120 125
 Cys Glu Gly Arg Ile Val Phe Val Ser Glu Asn Val Thr Ser Tyr Leu
 130 135 140
 Gly Tyr Asn Gln Glu Glu Leu Met Asn Thr Ser Val Tyr Ser Ile Leu
 145 150 155 160
 His Val Gly Asp His Ala Glu Phe Val Lys Asn Leu Leu Pro Lys Ser
 165 170 175
 Leu Val Asn Gly Val Pro Trp Pro Gln Glu Ala Thr Arg Arg Asn Ser
 180 185 190
 His Thr Phe Asn Cys Arg Met Leu Ile His Pro Pro Asp Glu Pro Gly
 195 200 205
 Thr Glu Asn Gln Glu Ala Cys Gln Arg Tyr Glu Val Met Gln Cys Phe
 210 215 220
 Thr Val Ser Gln Pro Lys Ser Ile Gln Glu Asp Gly Glu Asp Phe Gln
 225 230 235 240
 Ser Cys Leu Ile Cys Ile Ala Arg Arg Leu Pro Arg Pro Pro Ala Ile
 245 250 255
 Thr Gly Val Glu Ser Phe Met Thr Lys Gln Asp Thr Thr Gly Lys Ile
 260 265 270
 Ile Ser Ile Asp Thr Ser Ser Leu Arg Ala Ala Gly Arg Thr Gly Trp
 275 280 285
 Glu Asp Leu Val Arg Lys Cys Ile Tyr Ala Phe Phe Gln Pro Gln Gly
 290 295 300
 Arg Glu Pro Ser Tyr Ala Arg Gln Leu Phe Gln Glu Val Met Thr Arg
 305 310 315 320
 Gly Thr Ala Ser Ser Pro Ser Tyr Arg Phe Ile Leu Asn Asp Gly Thr
 325 330 335
 Met Leu Ser Ala His Thr Lys Cys Lys Leu Cys Tyr Pro Gln Ser Pro
 340 345 350
 Asp Met Gln Pro Phe Ile Met Gly Ile His Ile Ile Asp Arg Glu His
 355 360 365

Ser Gly Leu Ser Pro Gln Asp Asp Thr Asn Ser Gly Met Ser Ile Pro	370	375	380
Arg Val Asn Pro Ser Val Asn Pro Ser Ile Ser Pro Ala His Gly Val	385	390	395
Ala Arg Ser Ser Thr Leu Pro Pro Ser Asn Ser Asn Met Val Ser Thr	405	410	415
Arg Ile Asn Arg Gln Gln Ser Ser Asp Leu His Ser Ser Ser His Ser	420	425	430
Asn Ser Ser Asn Ser Gln Gly Ser Phe Gly Cys Ser Pro Gly Ser Gln	435	440	445
Ile Val Ala Asn Val Ala Leu Asn Lys Gly Gln Ala Ser Ser Gln Ser	450	455	460
Ser Lys Pro Ser Leu Asn Leu Asn Asn Pro Pro Met Glu Gly Thr Gly	465	470	475
Ile Ser Leu Ala Gln Phe Met Ser Pro Arg Arg Gln Val Thr Ser Gly	485	490	495
Leu Ala Thr Arg Pro Arg Met Pro Asn Asn Ser Phe Pro Pro Asn Ile	500	505	510
Ser Thr Leu Ser Ser Pro Val Gly Met Thr Ser Ser Ala Cys Asn Asn	515	520	525
Asn Asn Arg Ser Tyr Ser Asn Ile Pro Val Thr Ser Leu Gln Gly Met	530	535	540
Asn Glu Gly Pro Asn Asn Ser Val Gly Phe Ser Ala Ser Ser Pro Val	545	550	555
Leu Arg Gln Met Ser Ser Gln Asn Ser Pro Ser Arg Leu Asn Ile Gln	565	570	575
Pro Ala Lys Ala Glu Ser Lys Asp Asn Lys Glu Ile Ala Ser Thr Leu	580	585	590
Asn Glu Met Ile Gln Ser Asp Asn Ser Ser Ser Asp Gly Lys Pro Leu	595	600	605
Asp Ser Gly Leu Leu His Asn Asn Asp Arg Leu Ser Asp Gly Asp Ser	610	615	620
Lys Tyr Ser Gln Thr Ser His Lys Leu Val Gln Leu Leu Thr Thr Thr			
625	630	635	640
Ala Glu Gln Gln Leu Arg His Ala Asp Ile Asp Thr Ser Cys Lys Asp	645	650	655
Val Leu Ser Cys Thr Gly Thr Ser Asn Ser Ala Ser Ala Asn Ser Ser			
660	665	670	
Gly Gly Ser Cys Pro Ser Ser His Ser Ser Leu Thr Ala Arg His Lys	675	680	685
Ile Leu His Arg Leu Leu Gln Glu Gly Ser Pro Ser Asp Ile Thr Thr	690	695	700
Leu Ser Val Glu Pro Asp Lys Lys Asp Ser Ala Ser Thr Ser Val Ser	705	710	715
Val Thr Gly Gln Val Gln Gly Asn Ser Ser Ile Lys Leu Glu Leu Asp	725	730	735
Ala Ser Lys Lys Lys Glu Ser Lys Asp His Gln Leu Leu Arg Tyr Leu	740	745	750
Leu Asp Lys Asp Glu Lys Asp Leu Arg Ser Thr Pro Asn Leu Ser Leu	755	760	765
Asp Asp Val Lys Val Lys Val Glu Lys Lys Glu Gln Met Asp Pro Cys	770	775	780
Asn Thr Asn Pro Thr Pro Met Thr Lys Pro Thr Pro Glu Glu Ile Lys	785	790	795
Leu Glu Ala Gln Ser Gln Phe Thr Ala Asp Leu Asp Gln Phe Asp Gln	805	810	815
Leu Leu Pro Thr Leu Glu Lys Ala Ala Gln Leu Pro Gly Leu Cys Glu	820	825	830

Thr	Asp	Arg	Met	Asp	Gly	Ala	Val	Thr	Ser	Val	Thr	Ile	Lys	Ser	Glu	835	840	845
Ile	Leu	Pro	Ala	Ser	Leu	Gln	Ser	Ala	Thr	Ala	Arg	Pro	Thr	Ser	Arg	850	855	860
Leu	Asn	Arg	Leu	Pro	Glu	Leu	Glu	Leu	Glu	Ala	Ile	Asp	Asn	Gln	Phe	865	870	875
Gly	Gln	Pro	Gly	Thr	Gly	Asp	Gln	Ile	Pro	Trp	Thr	Asn	Asn	Thr	Val	885	890	895
Thr	Ala	Ile	Asn	Gln	Ser	Lys	Ser	Glu	Asp	Gln	Cys	Ile	Ser	Ser	Gln	900	905	910
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Glu	Lys	Ala	Leu	Leu	Glu	Gln	Leu	Val	Ser	Phe	Leu	Ser	Gly	Lys	Asp	930	935	940
Glu	Thr	Glu	Leu	Ala	Glu	Leu	Asp	Arg	Ala	Leu	Gly	Ile	Asp	Lys	Leu	945	950	955
Val	Gln	Gly	Gly	Gly	Leu	Asp	Val	Leu	Ser	Glu	Arg	Phe	Pro	Pro	Gln	965	970	975
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Gln	Gly	Met	Val	Arg	Gln	Lys	Pro	Ser	Leu	Gly	Thr	Met	Pro	Val	Gln	1010	1015	1020
Val	Thr	Pro	Pro	Arg	Gly	Ala	Phe	Ser	Pro	Gly	Met	Gly	Met	Gln	Pro	1025	1030	1035
Arg	Gln	Thr	Leu	Asn	Arg	Pro	Pro	Ala	Ala	Pro	Asn	Gln	Leu	Arg	Leu	1045	1050	1055
Gln	Leu	Gln	Gln	Arg	Leu	Gln	Gly	Gln	Gln	Gln	Leu	Ile	His	Gln	Asn	1060	1065	1070
Arg	Gln	Ala	Ile	Leu	Asn	Gln	Phe	Ala	Ala	Thr	Ala	Pro	Val	Gly	Ile	1075	1080	1085
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Asn	Ala	Gln	Met	Leu	Ala	Gln	Arg	Gln	Arg	Glu	Leu	Tyr	Ser	Gln	Gln	1105	1110	1115
His	Arg	Gln	Arg	Gln	Leu	Ile	Gln	Gln	Gln	Arg	Ala	Met	Leu	Met	Arg	1125	1130	1135
Gln	Gln	Ser	Phe	Gly	Asn	Asn	Leu	Pro	Pro	Ser	Ser	Gly	Leu	Pro	Val	1140	1145	1150
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Tyr	Pro	Pro	Asn	Tyr	Gly	Thr	Asn	Pro	Gly	Thr	Pro	Pro	Ala	Ser	Thr	1170	1175	1180
Ser	Pro	Phe	Ser	Gln	Leu	Ala	Ala	Asn	Pro	Glu	Ala	Ser	Leu	Ala	Asn	1185	1190	1195
Arg	Asn	Ser	Met	Val	Ser	Arg	Gly	Met	Thr	Gly	Asn	Ile	Gly	Gly	Gln	1205	1210	1215
Phe	Gly	Thr	Gly	Ile	Asn	Pro	Gln	Met	Gln	Gln	Asn	Val	Phe	Gln	Tyr	1220	1225	1230
Pro	Gly	Ala	Gly	Met	Val	Pro	Gln	Gly	Glu	Ala	Asn	Phe	Ala	Pro	Ser	1235	1240	1245
Leu	Ser	Pro	Gly	Ser	Ser	Met	Val	Pro	Met	Pro	Ile	Pro	Pro	Pro	Gln	1250	1255	1260
Ser	Ser	Leu	Leu	Gln	Gln	Thr	Pro	Pro	Ala	Ser	Gly	Tyr	Gln	Ser	Pro	1265	1270	1275
Asp	Met	Lys	Ala	Trp	Gln	Gln	Gly	Ala	Ile	Gly	Asn	Asn	Asn	Val	Phe	1285	1290	1295
Ser	Gln	Ala	Val	Gln	Asn	Gln	Pro	Thr	Pro	Ala	Gln	Pro	Gly	Val	Tyr	1300	1305	1310

Asn Asn Met Ser Ile Thr Val Ser Met Ala Gly Gly Asn Thr Asn Val
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